

From: Chan, Christina  
Sent: Tuesday, May 21, 2002 1:35 PM  
To: Davis, Minh-Tam; STIC-Biotech/ChemLib  
Subject: RE: Rush search request for 09583848

Please rush. Thanks Chris

-----Original Message-----

From: Davis, Minh-Tam  
Sent: Tuesday, May 21, 2002 12:03 PM  
To: Chan, Christina  
Subject: Rush search request for 09583848

Please use the parent case 08/037230 for searching.

Please search in commercial data base and in issued patent files:

Oligomer search for SEQ ID NO:18.

Since this case has priority date way back on 12/1991, is there anyway to print out sequences that are of older date?

Thanks.

MINH TAM DAVIS  
ART UNIT 1642, ROOM 8A01, MB 8E12  
305-2008

*full key to Mgr - 6*  
*only has priority date*  
*05/31/2000*  
*(date of filing)*  
*2 pp. t-p.*  
*42*  
*several*  
*claiming*  
*for complementary*  
*seq.*  
Point of Contact:  
Beverly Shears  
Technical Info. Specialist  
CM1 1E05 Tel: 308-4994

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST(where applic.)

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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# SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

Date completed: 05-24-92

Searcher: Beverly C4994

Terminal time: 20

Elapsed time: \_\_\_\_\_

CPU time: \_\_\_\_\_

Total time: 23

Number of Searches: \_\_\_\_\_

Number of Databases: 1

### Search Site

\_\_\_\_\_ STIC

\_\_\_\_\_ CM-1

\_\_\_\_\_ Pre-S

### Type of Search

\_\_\_\_\_ N.A. Sequence

\_\_\_\_\_ A.A. Sequence

\_\_\_\_\_ Structure

\_\_\_\_\_ Bibliographic

### Vendors

\_\_\_\_\_ IG

\_\_\_\_\_ STN

\_\_\_\_\_ Dialog

\_\_\_\_\_ APS

\_\_\_\_\_ Geninfo

\_\_\_\_\_ SDC

\_\_\_\_\_ DARC/Questel

☒ Other CGN

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 01:35:51 ; Search time 1787.52 Seconds  
(without alignments)  
2634.080 Million cell updates/sec

Title: US-08-037-230D-18  
Perfect score: 225  
Sequence: 1 TATTTCTTCTGTGATCTT.....GGACATGTCCTGAGGAG 225

Scoring table:  
OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0  
Searched: 1797656 seqs, 10463268293 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_on.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vl.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1	225	100.0	225	100.0	225	AR153509 Sequence
2	2	225	100.0	225	100.0	225	I36933 Sequence 18
3	3	157	69.8	945	6	6	AR167371 Sequence
4	4	157	69.8	945	6	6	HSU10339 Human MAGE-
5	5	157	69.8	1019	6	6	AR167377 Sequence
6	6	157	69.8	1019	6	6	D32076 Human mRNA
7	7	157	69.8	1362	6	6	AX019384 Sequence
8	8	157	69.8	3871	9	9	AX019384 Sequence
9	9	157	69.8	245077	9	9	AF002997 Homo sapi
10	10	74	32.9	1212	6	6	AX019380 Sequence
11	11	74	32.9	1353	6	6	AX019376 Sequence
12	12	74	32.9	1569	6	6	AX343855 Sequence
13	13	74	32.9	1640	6	6	AX343855 Sequence
14	14	74	32.9	1640	6	6	AR153502 Sequence
15	15	74	32.9	1663	9	9	I36926 Sequence 11
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17	17	74	32.9	1710	9	9	BC000340 Homo sapi
18	18	74	32.9	1715	9	9	BC017389 Homo sapi
19	19	74	32.9	1753	9	9	BC016803 Homo sapi
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22	22	74	32.9	4204	6	6	AR167370 Sequence
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29	29	36	16.0	1657	9	9	AX328164 Sequence
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78	23	10.2	166608	2	AC024727	Homo sapi	151	18	8.0	245	6	AX318626	AX318626 Sequence
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83	21	9.3	54	6	AX304457	Sequence	156	18	8.0	3179	6	AX179748	AX179748 Sequence
84	21	9.3	1801	9	BC012744	Homo sapi	157	18	8.0	4265	6	AR171862	AR171862 Sequence
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109	19	8.4	128361	9	AC034251	Homo sapi	182	18	8.0	145398	9	AC008132	AC008132 Homo sapi
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111	19	8.4	150159	2	AC018791	Human DNA	184	18	8.0	150781	2	AC091961	AC091961 Homo sapi
112	19	8.4	150236	2	HS101G11	Human DNA	185	18	8.0	151834	9	AP004195	AP004195 Homo sapi
113	19	8.4	151620	2	AC018589	Homo sapi	186	18	8.0	155256	2	AC109818	AC109818 Homo sapi
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126	19	8.4	169926	2	AC018593	Homo sapi	199	18	8.0	174736	9	AL355478	AL355478 Human DNA
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128	19	8.4	171401	9	AL592207	Homo sapi	201	18	8.0	180298	2	AL357633	AL357633 Homo sapi
129	19	8.4	172039	9	AC356741	Human DNA	202	18	8.0	180884	9	AC008018	AC008018 Homo sapi
130	19	8.4	174390	2	AC009522	Homo sapi	203	18	8.0	184406	9	AC009476	AC009476 Homo sapi
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132	19	8.4	180707	2	AC024460	Homo sapi	205	18	8.0	184600	30	AC026600	AC026600 Homo sapi
133	19	8.4	181663	9	AC010894	Homo sapi	206	18	8.0	186822	2	AC073235	AC073235 Homo sapi
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137	19	8.4	188460	9	AC010542	Homo sapi	210	18	8.0	190669	10	AL590429	AL590429 Mouse DNA
138	19	8.4	188854	10	AL626770	Mouse DNA	211	18	8.0	191735	2	AC079210	AC079210 Homo sapi
139	19	8.4	189534	2	AL354656	Homo sapi	212	18	8.0	195844	9	AL138751	AL138751 Human DNA
140	19	8.4	198821	2	AC018557	Homo sapi	213	18	8.0	195844	9	AC055757	AC055757 Homo sapi
141	19	8.4	190185	9	AC026464	Homo sapi	214	18	8.0	197637	2	AC055757	AC055757 Homo sapi
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143	19	8.4	192886	9	AC093887	Homo sapi	216	18	8.0	204674	2	AC099047	AC099047 Homo sapi
144	19	8.4	196568	2	AC026474	Homo sapi	217	18	8.0	208606	2	AC013548	AC013548 Mus muscu
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221	17	7.6	72	6	AX304455	AX304455 Sequence	c 294	17	7.6	35886	9	AC004035	AC004035 Homo sapi
222	17	7.6	339	6	AX246053	AX246053 Sequence	295	17	7.6	36156	9	AC004789	AC004789 Homo sapi
223	17	7.6	401	6	AX270177	AX270177 Sequence	296	17	7.6	36171	9	HSL21988	Z54246 Human DNA s
224	17	7.6	401	6	AX271708	AX271708 Sequence	c 297	17	7.6	36373	9	AL160252	AL160252 Human DNA
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227	17	7.6	458	1	AF267541	AF267541 Escherich	c 300	17	7.6	37139	9	AC006047	AC006047 Homo sapi
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229	17	7.6	458	1	AF267548	AF267548 Escherich	302	17	7.6	37425	3	U80842	U80842 Caenorhabdi
230	17	7.6	458	1	AF267549	AF267549 Escherich	303	17	7.6	37428	2	AC026327	AC026327 Homo sapi
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232	17	7.6	458	1	AF267554	AF267554 Escherich	c 305	17	7.6	39608	9	AC009004	AC009004 Homo sapi
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234	17	7.6	458	1	AF267556	AF267556 Escherich	307	17	7.6	39850	5	FRU010348	AF010348 Fugu rubr
235	17	7.6	458	1	AF267558	AF267558 Escherich	308	17	7.6	40395	9	AC009491	AC009491 Homo sapi
236	17	7.6	480	11	G34627	G34627 human SFS S	c 309	17	7.6	40438	9	AC087410	AC087410 Homo sapi
237	17	7.6	700	6	AX183308	AX183308 Sequence	c 310	17	7.6	40477	2	AC010514	AC010514 Homo sapi
238	17	7.6	819	1	ECAROE1	Y00710 Escherichia	c 311	17	7.6	40592	9	HSL191F1	Z68756 Human DNA s
239	17	7.6	913	33	AC081249	AC081249 Giardia i	c 312	17	7.6	40619	9	AC005222	AC005222 Homo sapi
240	17	7.6	1625	5	XELXDL	D10259 Xenopus mRN	c 313	17	7.6	40697	2	AC107874	AC107874 Homo sapi
241	17	7.6	1690	6	A87376	A87376 Sequence 7	c 314	17	7.6	41372	9	AL359082	AL359082 Human DNA
242	17	7.6	1690	9	HSRNUA114	Y10976 H.sapiens m	315	17	7.6	41459	9	AC004637	AC004637 Homo sapi
243	17	7.6	1824	9	HSUG2P	X01463 Human pseud	c 316	17	7.6	41618	9	AL355473	AL355473 Human DNA
244	17	7.6	1947	6	AX153510	AR153510 Sequence	c 317	17	7.6	41696	9	AC005932	AC005932 Homo sapi
245	17	7.6	1947	6	I36934	I36934 Sequence 19	c 318	17	7.6	42619	9	AC005615	AC005615 Homo sapi
246	17	7.6	1955	9	AF234236S55	AF234241 Homo sapi	319	17	7.6	43044	3	AC006730	AC006730 Caenorhab
247	17	7.6	1973	1	D85898	D85898 Streptomyces	c 320	17	7.6	43297	9	AC005578	AC005578 Homo sapi
248	17	7.6	2038	10	AB024538	AB024538 Mus muscu	c 321	17	7.6	43310	9	AC011519	AC011519 Homo sapi
249	17	7.6	2116	9	AK055733	AK055733 Homo sapi	322	17	7.6	43843	9	AC005796	AC005796 Homo sapi
250	17	7.6	2163	10	AB024539	AB024539 Mus muscu	c 323	17	7.6	43927	9	HSU69568	U69568 Human Xq28
251	17	7.6	2402	9	HUM25DC12	L43411 Homo sapien	c 324	17	7.6	44003	9	AF317635	AF317635 Homo sapi
252	17	7.6	2441	9	AB0606231	AB0606231 Macaca fa	325	17	7.6	44219	9	AC005512	AC005512 Homo sapi
253	17	7.6	2699	9	AB006713	AB006713 Homo sapi	c 326	17	7.6	44830	9	HSJ738A13	AL109801 Human DNA
254	17	7.6	2929	9	AK057698	AK057698 Homo sapi	327	17	7.6	44897	9	AF022794	AF022794 Homo sapi
255	17	7.6	3001	6	AX194618	AX194618 Sequence	c 328	17	7.6	45043	9	AF107045	AF107045 Homo sapi
256	17	7.6	3346	1	PSU81032	U81032 Pseudomonas	c 329	17	7.6	45754	9	AL139118	AL139118 Human DNA
257	17	7.6	3680	9	HSU10692	U10692 Human MAG-	c 330	17	7.6	45966	2	AC092309	AC092309 Homo sapi
258	17	7.6	4986	9	AL662856	AL662856 Human DNA	331	17	7.6	46463	9	HSE146D10	Z73420 Human DNA s
259	17	7.6	5142	9	AY030237	AY030237 Homo sapi	c 332	17	7.6	46508	9	AC073955	AC073955 Homo sapi
260	17	7.6	5215	1	WS0131242	AY031242 Wollinella	c 333	17	7.6	46619	9	AL513542	AL513542 Human DNA
261	17	7.6	6156	9	HUM20D8	D32063 Human gene	c 334	17	7.6	46791	9	AC004699	AC004699 Homo sapi
262	17	7.6	6210	9	AK024393	AK024393 Homo sapi	c 335	17	7.6	48119	9	AL139190	AL139190 Human DNA
263	17	7.6	9566	1	RPIW17A	L40585 xanthomonas	c 336	17	7.6	48478	2	AC026687	AC026687 Homo sapi
264	17	7.6	9995	1	AE008097	AE008097 Agrobacte	c 337	17	7.6	48763	9	AP000456	AP000456 Homo sapi
265	17	7.6	10184	9	AF410771	AF410771 Homo sapi	c 338	17	7.6	48860	9	AL136461	AL136461 Human DNA
266	17	7.6	10585	2	AC110465	AC110465 Rattus no	c 339	17	7.6	50348	9	HS81G23	AL035459 Human DNA
267	17	7.6	10747	1	AE000406	AE000406 Escherich	c 340	17	7.6	51803	9	AF176815	AF176815 Homo sapi
268	17	7.6	11201	1	AE001732	AE001732 Thermotog	c 341	17	7.6	51887	9	AL365193	AL365193 Human DNA
269	17	7.6	11365	9	AL591105	AL591105 Human DNA	c 342	17	7.6	52378	2	AC100849	AC100849 Homo sapi
270	17	7.6	11423	1	AE009132	AE009132 Agrobacte	c 343	17	7.6	53915	2	AC093147	Continuation (8 of
271	17	7.6	11616	1	AE009767	AE009767 Pyrobacul	c 344	17	7.6	53915	2	AC093147	AC093147 Homo sapi
272	17	7.6	13847	9	HSU7589B	Z69652 Human DNA s	345	17	7.6	54795	2	AC103701	AC103701 Homo sapi
273	17	7.6	14270	10	AF219626	AF219626 Mus muscu	346	17	7.6	54884	2	AC109519	AC109519 Homo sapi
274	17	7.6	14660	2	AC014636	AC014636 Drosophil	347	17	7.6	55591	2	AC1087813	AC1087813 Homo sapi
275	17	7.6	16043	9	HS36084	AL031008 Human DNA	348	17	7.6	56325	9	AL359712	AL359712 Human DNA
276	17	7.6	18700	9	AC087898	AC087898 Homo sapi	349	17	7.6	57759	9	AL37162	AL137162 Human chr
277	17	7.6	20539	9	HS349E10	AL022341 Human DNA	c 350	17	7.6	59297	2	CNS07EG8	AL5030327 Human chr
278	17	7.6	20873	9	AC079879	AC079879 Homo sapi	c 351	17	7.6	59378	2	AC100838	AC100838 Homo sapi
279	17	7.6	20890	9	HSU29895	U29895 Human 4-hyd	c 352	17	7.6	59765	9	AC005179	AC005179 Homo sapi
280	17	7.6	26078	9	AF376770	AF376770 Homo sapi	c 353	17	7.6	59816	2	AC107489	AC107489 Rattus no
281	17	7.6	27846	9	AC092689	AC092689 Homo sapi	c 354	17	7.6	60271	2	AC102866	AC102866 Homo sapi
282	17	7.6	27900	2	AC109090	AC109090 Rattus no	355	17	7.6	60352	2	AC102868	AC102868 Mus muscu
283	17	7.6	28519	9	HSJ563E14	AL117379 Human DNA	c 356	17	7.6	61336	2	AC107802	AC107802 Mus muscu
284	17	7.6	29963	9	HSJ56859	AL356859 Human DNA	357	17	7.6	61635	2	AC068928	AC068928 Homo sapi
285	17	7.6	30500	9	AC013481	AC013481 Homo sapi	358	17	7.6	62124	2	AC087580	AC087580 Homo sapi
286	17	7.6	30895	2	AC067716	AC067716 Homo sapi	c 359	17	7.6	62463	2	AC090300	AC090300 Homo sapi
287	17	7.6	32874	3	AE003172	AE003172 Drosophil	c 360	17	7.6	63017	9	AL157710	AL157710 Human DNA
288	17	7.6	33341	9	AC004750	AC004750 Homo sapi	c 361	17	7.6	63681	9	AL079398	AL079398 Homo sapi
289	17	7.6	33397	9	HSBA163M1	AL109802 Human DNA	362	17	7.6	63906	2	AC090793	AC090793 Homo sapi
290	17	7.6	33804	9	HS407A10	Z98883 Human DNA s	c 363	17	7.6	64114	2	AC084120	AC084120 Homo sapi
291	17	7.6	34768	9	AL138917	AL138917 Human DNA	c 364	17	7.6	64114	2	AC084120	AC084120 Homo sapi
292	17	7.6	35143	9	AP000229	AP000229 Homo sapi	c 365	17	7.6	64829	2	AC100338	AC100338 Mus muscu

c 366	17	7.6	65882	9	AL589734	Human DNA	AL589734	Human DNA	c 439	17	7.6	93923	2	AC090818	AC090818	Homo sapi
c 367	17	7.6	66000	2	AL391119	Human DNA	AL391119	Human DNA	c 440	17	7.6	94524	2	AC022115	AC022115	Homo sapi
c 368	17	7.6	66126	9	AC100959	Mus muscu	AC100959	Mus muscu	c 441	17	7.6	95655	2	AC110069	AC110069	Homo sapi
c 369	17	7.6	66206	2	AC023324	Homo sapi	AC023324	Homo sapi	c 442	17	7.6	96157	9	AL138789	AL138789	Human DNA
c 370	17	7.6	66248	2	AC030817	Homo sapi	AC030817	Homo sapi	c 443	17	7.6	96532	9	CNS07E06	CNS07E06	Human chr
c 371	17	7.6	66817	9	AC005201	Homo sapi	AC005201	Homo sapi	c 444	17	7.6	97101	2	AL450308	AL450308	Homo sapi
c 372	17	7.6	68369	2	AC093764	Homo sapi	AC093764	Homo sapi	c 445	17	7.6	97687	9	AL591403	AL591403	Human DNA
c 373	17	7.6	68476	2	AC021644_3	Continuation (4 of	Continuation (4 of	Continuation (4 of	c 446	17	7.6	97749	9	AC004906	AC004906	Homo sapi
c 374	17	7.6	68596	2	AC025118	Homo sapi	AC025118	Homo sapi	c 447	17	7.6	98247	2	AC025777	AC025777	Homo sapi
c 375	17	7.6	68872	2	AC103726	Homo sapi	AC103726	Homo sapi	c 448	17	7.6	98247	2	AC025777	AC025777	Homo sapi
c 376	17	7.6	68872	2	AC103726	Homo sapi	AC103726	Homo sapi	c 449	17	7.6	99594	2	AF263284	AF263284	Homo sapi
c 377	17	7.6	69027	9	AL596306	Human DNA	AL596306	Human DNA	c 450	17	7.6	99594	2	AF263284	AF263284	Homo sapi
c 378	17	7.6	69238	2	AC090784	Homo sapi	AC090784	Homo sapi	c 451	17	7.6	99682	9	HS452HI17	HS452HI17	Human DNA
c 379	17	7.6	69479	9	AL0088597	Homo sapi	AL0088597	Homo sapi	c 452	17	7.6	99864	2	AC023489	AC023489	Trypanoso
c 380	17	7.6	69535	9	AL583834	Human DNA	AL583834	Human DNA	c 453	17	7.6	100000	9	AP000144	AP000144	Homo sapi
c 381	17	7.6	69572	9	AC004769	Homo sapi	AC004769	Homo sapi	c 454	17	7.6	100000	9	AP000498	AP000498	Homo sapi
c 382	17	7.6	71192	2	AC101620	Mus muscu	AC101620	Mus muscu	c 455	17	7.6	100000	9	AP000509	AP000509	Homo sapi
c 383	17	7.6	71544	9	AC093792	Homo sapi	AC093792	Homo sapi	c 456	17	7.6	100000	9	AP000513	AP000513	Homo sapi
c 384	17	7.6	71602	9	AC092105	Homo sapi	AC092105	Homo sapi	c 457	17	7.6	100116	9	AL591178	AL591178	Human DNA
c 385	17	7.6	71607	9	AC073184	Homo sapi	AC073184	Homo sapi	c 458	17	7.6	100167	9	HSJ189G13	HSJ189G13	Human DNA
c 386	17	7.6	71631	2	AC068525	Homo sapi	AC068525	Homo sapi	c 459	17	7.6	100375	9	HS193B12	HS193B12	Human DNA
c 387	17	7.6	73199	2	AC023017	Homo sapi	AC023017	Homo sapi	c 460	17	7.6	100634	9	AP001594	AP001594	Human DNA
c 388	17	7.6	73459	2	AC023557	Homo sapi	AC023557	Homo sapi	c 461	17	7.6	101670	2	AC105714	AC105714	Rattus no
c 389	17	7.6	74393	2	AC021587	Homo sapi	AC021587	Homo sapi	c 462	17	7.6	102308	9	AC005231	AC005231	Homo sapi
c 390	17	7.6	75281	9	AL591893	Human DNA	AL591893	Human DNA	c 463	17	7.6	102387	9	AC022114	AC022114	Homo sapi
c 391	17	7.6	75525	9	HS071148	Human Xq28	HS071148	Human Xq28	c 464	17	7.6	102567	2	AC027694	AC027694	Homo sapi
c 392	17	7.6	76133	9	AL451081	Human DNA	AL451081	Human DNA	c 465	17	7.6	102624	9	AL161912	AL161912	Human DNA
c 393	17	7.6	76193	9	AL355877	Human DNA	AL355877	Human DNA	c 466	17	7.6	103565	9	AC005022	AC005022	Homo sapi
c 394	17	7.6	77087	9	AL590039	Human DNA	AL590039	Human DNA	c 467	17	7.6	103606	9	AC005004	AC005004	Homo sapi
c 395	17	7.6	77832	9	AL590039	Human DNA	AL590039	Human DNA	c 468	17	7.6	103720	9	AL161717	AL161717	Human DNA
c 396	17	7.6	78220	2	AC023212	Homo sapi	AC023212	Homo sapi	c 469	17	7.6	104309	9	AL138717	AL138717	Human DNA
c 397	17	7.6	78941	9	AC005591	Homo sapi	AC005591	Homo sapi	c 470	17	7.6	104357	9	AL392123	AL392123	Human DNA
c 398	17	7.6	79061	2	AC021357	Homo sapi	AC021357	Homo sapi	c 471	17	7.6	104660	9	AP000347	AP000347	Homo sapi
c 399	17	7.6	79170	9	AC026705	Homo sapi	AC026705	Homo sapi	c 472	17	7.6	104871	9	AC004584	AC004584	Homo sapi
c 400	17	7.6	79237	9	HS0J61M11	Human DNA	AL109624	Human DNA	c 473	17	7.6	105065	2	AC069132	AC069132	Homo sapi
c 401	17	7.6	79990	9	AC010457	Homo sapi	AC010457	Homo sapi	c 474	17	7.6	105118	9	AC019127	AC019127	Homo sapi
c 402	17	7.6	80272	2	HSJ491C16	Homo sapi	AL121976	Homo sapi	c 475	17	7.6	105138	9	AF124730	AF124730	Homo sapi
c 403	17	7.6	80824	9	AL513480	Human DNA	AL513480	Human DNA	c 476	17	7.6	105272	9	AL671884	AL671884	Human DNA
c 404	17	7.6	81057	9	AC080125	Homo sapi	AC080125	Homo sapi	c 477	17	7.6	105563	9	AC003983	AC003983	Human PAC
c 405	17	7.6	81268	2	AC016408	Homo sapi	AC016408	Homo sapi	c 478	17	7.6	106441	9	HSJ803J11	HSJ803J11	Human DNA
c 406	17	7.6	81419	9	AL133382	Human DNA	AL133382	Human DNA	c 479	17	7.6	106495	9	AC004864	AC004864	Homo sapi
c 407	17	7.6	81786	9	AC003002	Human DNA	AC003002	Human DNA	c 480	17	7.6	107104	9	HS1179L24	HS1179L24	Human DNA
c 408	17	7.6	81971	9	HS593CJ16	Human DNA	AL035702	Human DNA	c 481	17	7.6	107480	9	AC073118	AC073118	Homo sapi
c 409	17	7.6	82183	9	HSJ1037B9	Human DNA	AL117377	Human DNA	c 482	17	7.6	107603	9	HS934G17	HS934G17	Homo sapi
c 410	17	7.6	84335	2	AC018387	Homo sapi	AC018387	Homo sapi	c 483	17	7.6	108373	9	AL358034	AL358034	Human DNA
c 411	17	7.6	84570	9	AL359552	Human DNA	AL359552	Human DNA	c 484	17	7.6	108793	9	AL137839	AL137839	Human DNA
c 412	17	7.6	84707	9	AL355475	Human DNA	AL355475	Human DNA	c 485	17	7.6	108845	1	U66917	U66917	Pseudomonas
c 413	17	7.6	84879	9	AL590325	Human DNA	AL590325	Human DNA	c 486	17	7.6	108902	2	AC011430	AC011430	Homo sapi
c 414	17	7.6	85084	9	AB042297	Homo sapi	AB042297	Homo sapi	c 487	17	7.6	108922	9	AC016870	AC016870	Homo sapi
c 415	17	7.6	86381	2	AL360077	Homo sapi	AL360077	Homo sapi	c 488	17	7.6	109176	9	AL161911	AL161911	Human DNA
c 416	17	7.6	86554	2	AC090280	Homo sapi	AC090280	Homo sapi	c 489	17	7.6	109867	9	AC004898	AC004898	Homo sapi
c 417	17	7.6	86829	9	AC011382	Homo sapi	AC011382	Homo sapi	c 490	17	7.6	110000	1	EC00W67_2	EC00W67_2	Continuation (3 of
c 418	17	7.6	87156	2	AC068450	Homo sapi	AC068450	Homo sapi	c 491	17	7.6	110000	2	AC003656_6	AC003656_6	Continuation (7 of
c 419	17	7.6	87434	9	HSJ297357	Homo sapi	HSJ297357	Homo sapi	c 492	17	7.6	110291_1	2	AC105291_1	AC105291_1	Continuation (2 of
c 420	17	7.6	87739	2	AL592150	Homo sapi	AL592150	Homo sapi	c 493	17	7.6	110000	2	AL139235_2	AL139235_2	Continuation (3 of
c 421	17	7.6	87789	9	AL133270	Human DNA	AL133270	Human DNA	c 494	17	7.6	110000	2	AL354714_5	AL354714_5	Continuation (6 of
c 422	17	7.6	87925	2	AC005318	Homo sapi	AC005318	Homo sapi	c 495	17	7.6	110000	2	AL354792_0	AL354792_0	Continuation (4 of
c 423	17	7.6	87944	2	AC023662	Homo sapi	AC023662	Homo sapi	c 496	17	7.6	110000	2	AL670455_3	AL670455_3	Continuation (4 of
c 424	17	7.6	88071	9	AC002316	Homo sapi	AC002316	Homo sapi	c 497	17	7.6	110013	2	AC046157	AC046157	Homo sapi
c 425	17	7.6	88473	9	AF191071	Homo sapi	AF191071	Homo sapi	c 498	17	7.6	110535	9	AC005091	AC005091	Homo sapi
c 426	17	7.6	88718	2	AC097545	Rattus no	AC097545	Rattus no	c 499	17	7.6	110716	2	AC008717	AC008717	Homo sapi
c 427	17	7.6	89044	2	AC099680	Homo sapi	AC099680	Homo sapi	c 500	17	7.6	110820	9	AL596285	AL596285	Human DNA
c 428	17	7.6	89448	9	AC005067	Homo sapi	AC005067	Homo sapi	c 501	17	7.6	110965	9	AC026697	AC026697	Homo sapi
c 429	17	7.6	89665	9	AC063976	Homo sapi	AC063976	Homo sapi	c 502	17	7.6	111037	2	AC090067	AC090067	Homo sapi
c 430	17	7.6	89862	9	AC007164	Homo sapi	AC007164	Homo sapi	c 503	17	7.6	111076	2	AP003162	AP003162	Homo sapi
c 431	17	7.6	90399	2	AL162405	Homo sapi	AL162405	Homo sapi	c 504	17	7.6	111118	9	HSAC000112	HSAC000112	Human PAC
c 432	17	7.6	91355	9	AL391417	Human DNA	AL391417	Human DNA	c 505	17	7.6	111560	9	AC016940	AC016940	Homo sapi
c 433	17	7.6	91365	9	HS116F5	Human DNA s	Z93244	Human DNA s	c 506	17	7.6	113019	2	AC090141	AC090141	Homo sapi
c 434	17	7.6	92569	9	AL353688	Human DNA	AL353688	Human DNA	c 507	17	7.6	113212	9	AL513355	AL513355	Human DNA
c 435	17	7.6	92636	9	AC005251	Homo sapi	AC005251	Homo sapi	c 508	17	7.6	113879	9	AC011904	AC011904	Homo sapi
c 436	17	7.6	92679	2	AC098804	Homo sapi	AC098804	Homo sapi	c 509	17	7.6	113929	2	AF196969	AF196969	Homo sapi
c 437	17	7.6	93033	2	AP000644	Homo sapi	AP000644	Homo sapi	c 510	17	7.6	113982	2	AF192303	AF192303	Homo sapi
c 438	17	7.6	93567	2	AP004179	Oryza sat	AP004179	Oryza sat	c 511	17	7.6	114149	9	AC022083	AC022083	Homo sapi



512	17	7.6 114434	9	AC0933728	AC093728 Homo sapi	585	17	7.6 131274	9	AC069506	Homo sapi
513	17	7.6 115408	2	AC068848	AC068848 Homo sapi	c 586	17	7.6 131928	9	AC091738	Homo sapi
c 514	17	7.6 116014	9	AL353772	AL353772 Human DNA	587	17	7.6 132068	9	AC006965	Homo sapi
c 515	17	7.6 116079	9	AL365271	AL365271 Human DNA	c 588	17	7.6 132327	9	AL158209	Human DNA
c 516	17	7.6 116368	9	HS1112F19	AL034420 Human DNA	c 589	17	7.6 132433	9	HS0210B1	Human DNA
c 517	17	7.6 116513	9	HS487J7	AL008730 Human DNA	c 590	17	7.6 133687	2	AC002093	Homo sapi
c 518	17	7.6 116664	9	HS1191N16	AL118501 Human DNA	c 591	17	7.6 133786	2	AC091839	Homo sapi
c 519	17	7.6 117521	2	AC023784	AC023784 Homo sapi	c 592	17	7.6 133814	2	AC027550	Homo sapi
c 520	17	7.6 117911	9	HS117P19	286061 Human DNA s	c 593	17	7.6 133922	9	AC023469	Homo sapi
c 521	17	7.6 118030	2	AP000667	AP000667 Homo sapi	c 594	17	7.6 133965	9	AF064861	Homo sapi
c 522	17	7.6 118068	9	HS356798	AL356798 Human DNA	c 595	17	7.6 134184	9	AC095044	Homo sapi
c 523	17	7.6 118153	9	HS249C1	AL022154 Human DNA	c 596	17	7.6 134347	9	AL356295	Human DNA
c 524	17	7.6 118440	9	AC016939	AC016939 Homo sapi	c 597	17	7.6 134882	9	AC008622	Homo sapi
c 525	17	7.6 118447	2	AC093508	AC093508 Homo sapi	c 598	17	7.6 134890	2	AC009793	Homo sapi
c 526	17	7.6 118447	2	AC093508	AC093508 Homo sapi	c 599	17	7.6 135405	9	AC000025	Homo sapi
c 527	17	7.6 118492	2	AC020548	AC020548 Homo sapi	600	17	7.6 135637	9	AP003400	Homo sapi
c 528	17	7.6 118499	9	AL390722	AL390722 Human DNA	601	17	7.6 135648	9	AC004069	Homo sapi
c 529	17	7.6 118906	9	AL353583	AL353583 Human DNA	c 602	17	7.6 135666	2	AL513013	Homo sapi
c 530	17	7.6 118995	9	AC005368	AC005368 Homo sapi	c 603	17	7.6 136105	2	AL100740	Mus muscu
c 531	17	7.6 119235	2	AC011817	AC011817 Homo sapi	c 604	17	7.6 136168	9	HS1049G11	Human DNA
c 532	17	7.6 119236	9	CNS05TEX	AL359402 Human chr	605	17	7.6 136587	9	AL445309	Human DNA
c 533	17	7.6 119395	9	AL139189	AL139189 Human DNA	606	17	7.6 136778	2	AC108376	Pan trogl
c 534	17	7.6 119460	9	AL590431	AL590431 Human DNA	607	17	7.6 136932	9	AC068035	Homo sapi
c 535	17	7.6 119502	9	AL157781	AL157781 Human DNA	c 608	17	7.6 137271	9	AC004552	Homo sapi
c 536	17	7.6 120134	2	AC008034	AC008034 Homo sapi	609	17	7.6 137610	9	AC013478	Homo sapi
c 537	17	7.6 120466	9	AC093813	AC093813 Homo sapi	610	17	7.6 137730	9	HS365E2	Human DNA
c 538	17	7.6 120871	9	AP001054	AP001054 Homo sapi	611	17	7.6 137737	9	AC010378	Homo sapi
c 539	17	7.6 121200	9	HS135L22	AL031767 Human DNA	c 612	17	7.6 137833	9	CNS01DV6	Human chr
c 540	17	7.6 121702	9	AC007622	AC007622 Homo sapi	c 613	17	7.6 137886	30	AC027581	Homo sapi
c 541	17	7.6 121788	2	AC022420	AC022420 Homo sapi	614	17	7.6 137950	9	AC022137	Homo sapi
c 542	17	7.6 121800	9	AL359924	AL359924 Human DNA	c 615	17	7.6 138021	9	AC090820	Homo sapi
c 543	17	7.6 121949	9	AL157772	AL157772 Human DNA	c 616	17	7.6 138224	9	AC096562	Homo sapi
c 544	17	7.6 122001	2	AC107375	AC107375 Homo sapi	617	17	7.6 138329	2	AC093226-	Homo sapi
c 545	17	7.6 122102	9	AC010468	AC010468 Homo sapi	618	17	7.6 138735	2	AC012031	Homo sapi
c 546	17	7.6 122103	9	HS291J710	293017 Human DNA s	619	17	7.6 138752	9	AL161627	Human DNA
c 547	17	7.6 122302	9	AC003982	AC003982 Homo sapi	620	17	7.6 139607	2	AC104796	Homo sapi
c 548	17	7.6 122638	9	AB001523	AB001523 Homo sapi	c 621	17	7.6 139627	2	AL357117	Human DNA
c 549	17	7.6 122717	2	AP001186	AP001186 Homo sapi	c 622	17	7.6 140007	2	AC091896	Homo sapi
c 550	17	7.6 122913	9	AL139404	AL139404 Human DNA	c 623	17	7.6 140042	2	AC073038	Homo sapi
c 551	17	7.6 123062	2	AC099359	AC099359 Rattus no	c 624	17	7.6 140292	9	CNS01DU8	Human chr
c 552	17	7.6 123170	2	AL138792	AL138792 Homo sapi	c 625	17	7.6 140334	9	AC021802	Homo sapi
c 553	17	7.6 123507	2	AC099721	AC099721 Homo sapi	626	17	7.6 140378	2	AC068205	Homo sapi
c 554	17	7.6 123554	9	AB023049	AB023049 Homo sapi	627	17	7.6 140403	2	AC109444	Homo sapi
c 555	17	7.6 123631	9	HS22F01	AL109967 Homo sapi	c 628	17	7.6 140706	2	AC098106	Rattus no
c 556	17	7.6 123693	9	AL152853	AL152853 Human DNA	c 629	17	7.6 140874	2	AC027227	Homo sapi
c 557	17	7.6 123778	9	AC069294	AC069294 Homo sapi	c 630	17	7.6 140944	2	AC096136	Rattus no
c 558	17	7.6 123830	9	HS500L14	AL023583 Human DNA	c 631	17	7.6 140974	9	AC068533	Homo sapi
c 559	17	7.6 124001	9	HS886K2	AL031295 Human DNA	c 632	17	7.6 141371	9	AC010319	Homo sapi
c 560	17	7.6 124437	9	AL139125	AL139125 Human DNA	c 633	17	7.6 141372	2	AC011779	Homo sapi
c 561	17	7.6 124635	9	AP000593	AP000593 Homo sapi	c 634	17	7.6 141701	2	AC024541	Homo sapi
c 562	17	7.6 124699	9	AL590617	AL590617 Human DNA	c 635	17	7.6 141779	9	AC002377	Human PAC
c 563	17	7.6 124975	2	AC107063	AC107063 Bos tauru	c 636	17	7.6 142123	2	AC068890	Homo sapi
c 564	17	7.6 125291	9	AP000646	AP000646 Homo sapi	c 637	17	7.6 142215	2	AC092066	Homo sapi
c 565	17	7.6 125553	9	AL513263	AL513263 Human DNA	c 638	17	7.6 142254	2	AC094110	Pan trogl
c 566	17	7.6 125746	9	AC010589	AC010589 Homo sapi	c 639	17	7.6 142277	2	AC016204	Homo sapi
c 567	17	7.6 126807	9	HS391O22	AL031577 Human DNA	c 640	17	7.6 142441	2	HSJ344H20	Homo sapi
c 568	17	7.6 127405	9	HS1119A7	AL022313 Human DNA	c 641	17	7.6 142494	9	AL137119	Human DNA
c 569	17	7.6 127905	9	AL513550	AL513550 Human DNA	c 642	17	7.6 142669	2	AC018912	Homo sapi
c 570	17	7.6 128435	9	AL590411	AL590411 Human DNA	c 643	17	7.6 142803	9	AL592525	Human DNA
c 571	17	7.6 128683	2	AF286886	AF286886 Homo sapi	c 644	17	7.6 142933	9	AL513102	Human DNA
c 572	17	7.6 128769	2	AL139261	AL139261 Homo sapi	c 645	17	7.6 142938	2	AC104184	Homo sapi
c 573	17	7.6 129011	2	AC091860	AC091860 Homo sapi	c 646	17	7.6 143163	9	HSBK21C21	Human DNA
c 574	17	7.6 129048	9	AC020931	AC020931 Homo sapi	c 647	17	7.6 143428	9	AL162587	Human DNA
c 575	17	7.6 129169	2	AC032038	AC032038 Homo sapi	c 648	17	7.6 143436	9	AC004456	Homo sapi
c 576	17	7.6 129225	9	AC026765	AC026765 Homo sapi	c 649	17	7.6 143591	2	AC092197	Homo sapi
c 577	17	7.6 129504	9	AL445469	AL445469 Human DNA	c 650	17	7.6 143676	2	AC026435	Homo sapi
c 578	17	7.6 129727	9	AC084381	AC084381 Homo sapi	c 651	17	7.6 143683	9	AL356376	Human DNA
c 579	17	7.6 129949	2	AC022940	AC022940 Homo sapi	c 652	17	7.6 143754	2	AL359093	Homo sapi
c 580	17	7.6 129949	2	AC022940	AC022940 Homo sapi	c 653	17	7.6 143840	30	AC027210	Homo sapi
c 581	17	7.6 130639	9	AL356489	AL356489 Human DNA	c 654	17	7.6 143893	2	AC010766	Homo sapi
c 582	17	7.6 130647	9	AL157385	AL157385 Human DNA	c 655	17	7.6 143952	9	AL589987	Human DNA
c 583	17	7.6 130715	9	AL391557	AL391557 Human DNA	c 656	17	7.6 144233	2	AC068103	Homo sapi
c 584	17	7.6 130754	2	AC008508	AC008508 Homo sapi	c 657	17	7.6 144434	2	AC099534	Homo sapi

c 658	17	7.6 144542	9	AC015819	AC015819 Homo sapi	c 731	17	7.6 152058	2	AC025232	AC025232 Homo sapi
c 659	17	7.6 144555	2	AC037451	AC037451 Homo sapi	c 732	17	7.6 152224	2	AC007933	AC007933 Homo sapi
c 660	17	7.6 144676	9	HS390013	284469 Human DNA s	733	17	7.6 152269	2	AL591024	AL591024 Homo sapi
c 661	17	7.6 144967	2	AC008963	AC008963 Homo sapi	734	17	7.6 152573	9	AL445202	AL445202 Human DNA
c 662	17	7.6 145100	2	AC024641	AC024641 Homo sapi	735	17	7.6 152573	9	HSJ534K7	AL109925 Human DNA
c 663	17	7.6 145101	2	AC021775	AC021775 Homo sapi	736	17	7.6 152659	9	AL591503	AL591503 Human DNA
c 664	17	7.6 145152	2	AC005805	AC005805 Homo sapi	737	17	7.6 152664	2	AC012158	AC012158 Homo sapi
c 665	17	7.6 145253	9	AC006329	AC006329 Homo sapi	c 738	17	7.6 152861	2	AC023451	AC023451 Homo sapi
c 666	17	7.6 145329	2	AC055850	AC055850 Homo sapi	739	17	7.6 153088	2	AC046135	AC046135 Homo sapi
c 667	17	7.6 145414	9	HS78F24	AL022336 Human DNA	740	17	7.6 153094	2	AC096715	AC096715 Homo sapi
c 668	17	7.6 145414	9	HS392M18	AL121897 Human DNA	c 741	17	7.6 153108	9	AL355273	AL355273 Human DNA
c 669	17	7.6 145414	9	HS392M18	AL121897 Human DNA	742	17	7.6 153154	2	AL669876	AL669876 Homo sapi
c 670	17	7.6 145442	9	AC004859	AC004859 Homo sapi	c 743	17	7.6 153168	9	AC011974	AC011974 Homo sapi
c 671	17	7.6 145630	9	AL512622	AL512622 Human DNA	c 744	17	7.6 153218	2	AC015920	AC015920 Homo sapi
c 672	17	7.6 145831	6	AX330137	AX330137 Sequence	745	17	7.6 153241	9	AC023510	AC023510 Homo sapi
c 673	17	7.6 145831	6	AX334634	AX334634 Sequence	746	17	7.6 153381	2	AP001990	AP001990 Homo sapi
c 674	17	7.6 145831	6	AX336416	AX336416 Sequence	747	17	7.6 153392	9	AL133548	AL133548 Human DNA
c 675	17	7.6 145831	6	AX337041	AX337041 Sequence	748	17	7.6 153539	2	AL591168	AL591168 Homo sapi
c 676	17	7.6 145831	9	HUAF001548	AF001548 Human Chr	749	17	7.6 153629	9	AC092325	AC092325 Homo sapi
c 677	17	7.6 146124	9	AL358938	AL358938 Human DNA	750	17	7.6 153778	2	AC087528	AC087528 Homo sapi
c 678	17	7.6 146278	9	AL356413	AL356413 Human DNA	751	17	7.6 153860	2	AC016301	AC016301 Homo sapi
c 679	17	7.6 146312	2	AC008769	AC008769 Homo sapi	752	17	7.6 154036	9	AC008068	AC008068 Homo sapi
c 680	17	7.6 146677	2	AC016275	AC016275 Homo sapi	c 753	17	7.6 154323	2	AC026033	AC026033 Homo sapi
c 681	17	7.6 146776	2	AC093486	AC093486 Homo sapi	754	17	7.6 154394	9	HS34B21	AL031778 Human DNA
c 682	17	7.6 146805	2	AL450424	AL450424 Homo sapi	c 755	17	7.6 154533	2	AC018533	AC018533 Homo sapi
c 683	17	7.6 147259	2	AC019248	AC019248 Homo sapi	756	17	7.6 154499	2	AC031987	AC031987 Homo sapi
c 684	17	7.6 147260	2	AC016340	AC016340 Homo sapi	757	17	7.6 154526	2	AL592111	AL592111 Homo sapi
c 685	17	7.6 147260	2	AC016340	AC016340 Homo sapi	c 758	17	7.6 154584	9	AC015641	AC015641 Homo sapi
c 686	17	7.6 147964	2	AC008158	AC008158 Homo sapi	c 759	17	7.6 154597	9	AP004295	AP004295 Homo sapi
c 687	17	7.6 148018	2	HSJ613A2	AL121990 Homo sapi	c 760	17	7.6 154616	2	AC067772	AC067772 Homo sapi
c 688	17	7.6 148049	9	HS3300188	AL300188 Homo sapi	c 761	17	7.6 154664	9	AC025362	AC025362 Homo sapi
c 689	17	7.6 148081	9	AB045361	AB045361 Homo sapi	c 762	17	7.6 154744	2	AC079114	AC079114 Homo sapi
c 690	17	7.6 148164	2	AC0105105	AL105105 Homo sapi	763	17	7.6 154897	9	AL162272	AL162272 Human DNA
c 691	17	7.6 148430	9	AL139328	AL139328 Human DNA	c 764	17	7.6 154904	2	AC002395	AC002395 Homo sapi
c 692	17	7.6 148487	2	AC011593	AC011593 Homo sapi	765	17	7.6 155022	2	AC002395	AC002395 Homo sapi
c 693	17	7.6 148507	9	AC008784	AC008784 Homo sapi	c 766	17	7.6 155053	2	AC015795	AC015795 Homo sapi
c 694	17	7.6 148507	9	AC008784	AC008784 Homo sapi	767	17	7.6 155106	2	AC104069	AC104069 Homo sapi
c 695	17	7.6 148598	9	HSBA51C14	AL121875 Human DNA	c 768	17	7.6 155186	2	AC068373	AC068373 Homo sapi
c 696	17	7.6 148653	2	AC110281	AC110281 Homo sapi	769	17	7.6 155195	2	AC092518	AC092518 Felis cat
c 697	17	7.6 148752	9	AL596225	AL596225 Human DNA	770	17	7.6 155332	9	AC040900	AC040900 Homo sapi
c 698	17	7.6 148772	2	AC055826	AC055826 Homo sapi	c 771	17	7.6 155405	9	AC009812	AC009812 Homo sapi
c 699	17	7.6 149133	2	AC079089	AC079089 Homo sapi	c 772	17	7.6 155667	2	AC067911	AC067911 Homo sapi
c 700	17	7.6 149202	2	AC022160	AC022160 Homo sapi	c 773	17	7.6 155770	2	AC092381	AC092381 Homo sapi
c 701	17	7.6 149214	2	AC026535	AC026535 Homo sapi	774	17	7.6 155816	2	AC091927	AC091927 Homo sapi
c 702	17	7.6 149308	9	AC005527	AC005527 Homo sapi	775	17	7.6 155824	2	AC087296	AC087296 Homo sapi
c 703	17	7.6 149321	9	HS106120	AL079295 Human DNA	c 776	17	7.6 156277	9	AC026795	AC026795 Homo sapi
c 704	17	7.6 149409	9	AC004081	AC004081 Homo sapi	777	17	7.6 156371	2	AC104116	AC104116 Homo sapi
c 705	17	7.6 149618	9	AP000556	AP000556 Homo sapi	778	17	7.6 156386	2	AC009171	AC009171 Homo sapi
c 706	17	7.6 149705	9	AC074362	AC074362 Homo sapi	779	17	7.6 156473	2	AC097261	AC097261 Homo sapi
c 707	17	7.6 149901	2	AC068563	AC068563 Homo sapi	780	17	7.6 156481	2	AL392107	AL392107 Homo sapi
c 708	17	7.6 150036	9	AP000557	AP000557 Homo sapi	781	17	7.6 156542	9	AC018618	AC018618 Homo sapi
c 709	17	7.6 150193	2	AC009641	AC009641 Homo sapi	782	17	7.6 156596	2	AL445070	AL445070 Homo sapi
c 710	17	7.6 150332	9	AC004921	AC004921 Homo sapi	783	17	7.6 156700	2	AC027051	AC027051 Homo sapi
c 711	17	7.6 150354	9	AC091920	AC091920 Homo sapi	784	17	7.6 156733	9	AP000640	AP000640 Homo sapi
c 712	17	7.6 150520	9	AL136305	AL136305 Human DNA	785	17	7.6 156748	2	AC015481	AC015481 Homo sapi
c 713	17	7.6 150581	9	AP003693	AP003693 Homo sapi	786	17	7.6 156833	9	AC018712	AC018712 Homo sapi
c 714	17	7.6 150587	2	AC005973	AC005973 Homo sapi	c 787	17	7.6 156836	2	AC068059	AC068059 Homo sapi
c 715	17	7.6 150759	2	AP001130	AP001130 Homo sapi	788	17	7.6 157007	2	AC066599	AC066599 Homo sapi
c 716	17	7.6 150855	2	AC021258	AC021258 Homo sapi	c 789	17	7.6 157023	2	AC107018	AC107018 Homo sapi
c 717	17	7.6 150896	2	AC098980	AC098980 Rattus no	c 790	17	7.6 157067	9	AC010163	AC010163 Homo sapi
c 718	17	7.6 150902	2	AC018391	AC018391 Homo sapi	791	17	7.6 157086	9	AP000552	AP000552 Homo sapi
c 719	17	7.6 150947	2	AC087370	AC087370 Homo sapi	c 792	17	7.6 157116	9	AC009054	AC009054 Homo sapi
c 720	17	7.6 151008	2	AC035146	AC035146 Homo sapi	793	17	7.6 157225	2	AC105765	AC105765 Homo sapi
c 721	17	7.6 151008	2	AC035146	AC035146 Homo sapi	794	17	7.6 157321	9	AC004912	AC004912 Homo sapi
c 722	17	7.6 151026	9	AC005915	AC005915 Homo sapi	795	17	7.6 157336	2	AC079787	AC079787 Homo sapi
c 723	17	7.6 151182	9	AL611942	AL611942 Human DNA	c 796	17	7.6 157337	9	AC009163	AC009163 Homo sapi
c 724	17	7.6 151228	9	AL662800	AL662800 Human DNA	c 797	17	7.6 157390	2	AC025366	AC025366 Homo sapi
c 725	17	7.6 151294	2	AC069364	AC069364 Homo sapi	c 798	17	7.6 157402	2	AC034161	AC034161 Homo sapi
c 726	17	7.6 151341	2	AC019297	AC019297 Homo sapi	c 799	17	7.6 157463	9	AC091529	AC091529 Homo sapi
c 727	17	7.6 151552	9	AL355863	AL355863 Human DNA	c 800	17	7.6 157478	2	AC015515	AC015515 Homo sapi
c 728	17	7.6 151736	2	AC024439	AC024439 Homo sapi	801	17	7.6 157548	2	AC026637	AC026637 Homo sapi
c 729	17	7.6 151801	9	AC008906	AC008906 Homo sapi	c 802	17	7.6 157565	2	AL160156	AL160156 Homo sapi
730	17	7.6 151881	9	AC008629	AC008629 Homo sapi	803	17	7.6 157657	2	AL074243	AL074243 Homo sapi

804	17	7.6 157662	9	AL139035	Human DNA	877	17	7.6 162209	9	CNS01RTH	AL163195	Human chr
805	17	7.6 157779	9	AL590624	Human DNA	878	17	7.6 162380	2	AC018851	AC018851	Homo sapi
806	17	7.6 157813	9	AC005535	Homo sapi	879	17	7.6 162416	9	AC026882	AC026882	Homo sapi
807	17	7.6 157814	9	AC037460	Homo sapi	880	17	7.6 162591	9	AL391839	AL391839	Human DNA
808	17	7.6 157819	30	AL160277	Human DNA	881	17	7.6 162591	9	AL391839	AL391839	Human DNA
809	17	7.6 157834	9	AC022931	Homo sapi	882	17	7.6 162765	2	HS467L1	298884	Human DNA s
810	17	7.6 157872	9	AC007850	Homo sapi	883	17	7.6 162765	2	AL591362	AL591362	Homo sapi
811	17	7.6 158073	9	AC069298	Homo sapi	884	17	7.6 162765	2	AL591362	AL591362	Homo sapi
812	17	7.6 158099	9	CNS05THC	Homo sapi	885	17	7.6 162797	2	AC098981	AC098981	Rattus no
813	17	7.6 158214	9	CNS05THC	Human chr	886	17	7.6 162935	2	AC013486	AC013486	Homo sapi
814	17	7.6 158338	9	AC024720	Homo sapi	887	17	7.6 162949	2	AC068029	AC068029	Homo sapi
815	17	7.6 158427	9	AC002553	Homo sapi	888	17	7.6 162951	2	AC084094	AC084094	Homo sapi
816	17	7.6 158591	9	AC010188	Homo sapi	889	17	7.6 162968	2	AC069303	AC069303	Homo sapi
817	17	7.6 158700	2	AC027643	Homo sapi	890	17	7.6 162973	2	AC016307	AC016307	Homo sapi
818	17	7.6 158798	9	U82696	Homo sapien	891	17	7.6 162978	9	AC021070	AC021070	Homo sapi
819	17	7.6 158902	2	AC013778	Homo sapi	892	17	7.6 162986	9	CNS05TEB	AL163953	Human chr
820	17	7.6 159013	2	AP000931	Homo sapi	893	17	7.6 163005	2	AP001522	AP001522	Homo sapi
821	17	7.6 159057	2	AC023995	Homo sapi	894	17	7.6 163057	2	AC012419	AC012419	Homo sapi
822	17	7.6 159110	9	AL355296	Human DNA	895	17	7.6 163108	9	AL450998	AL450998	Human DNA
823	17	7.6 159146	2	AL592424	Homo sapi	896	17	7.6 163137	2	AP001458	AP001458	Homo sapi
824	17	7.6 159209	2	AC079097	Homo sapi	897	17	7.6 163192	2	AC079751	AC079751	Homo sapi
825	17	7.6 159254	2	AC084394	Homo sapi	898	17	7.6 163332	9	AC004821	AC004821	Homo sapi
826	17	7.6 159273	2	AC025001	Homo sapi	899	17	7.6 163338	9	AL162426	AL162426	Human DNA
827	17	7.6 159294	9	AL357506	Human DNA	900	17	7.6 163392	9	AL589765	AL589765	Human DNA
828	17	7.6 159366	2	AC073595	Homo sapi	901	17	7.6 163401	2	AC073251	AC073251	Homo sapi
829	17	7.6 159409	2	AC092900	Homo sapi	902	17	7.6 163521	2	AC108040	AC108040	Homo sapi
830	17	7.6 159433	2	AC021859	Homo sapi	903	17	7.6 163599	9	HS081D8	AL109933	Human DNA
831	17	7.6 159516	2	AC048330	Homo sapi	904	17	7.6 163632	9	AL513185	AL513185	Human DNA
832	17	7.6 159610	2	AC012137	Homo sapi	905	17	7.6 163660	2	AC046165	AC046165	Homo sapi
833	17	7.6 159692	9	AC013693	Homo sapi	906	17	7.6 163757	2	AC092418	AC092418	Homo sapi
834	17	7.6 159698	2	AC027269	Homo sapi	907	17	7.6 163807	2	AC018934	AC018934	Homo sapi
835	17	7.6 159707	2	AL365403	Homo sapi	908	17	7.6 163828	2	AL662867	AL662867	Homo sapi
836	17	7.6 159723	2	AC021862	Homo sapi	909	17	7.6 163852	9	AC015971	AC015971	Homo sapi
837	17	7.6 159765	2	AL359533	Mus muscu	910	17	7.6 164028	9	AC004890	AC004890	Homo sapi
838	17	7.6 160015	9	AC092183	Homo sapi	911	17	7.6 164144	9	AL591704	AL591704	Human DNA
839	17	7.6 160127	2	AC068977	Homo sapi	912	17	7.6 164220	30	AC024130	AC024130	Homo sapi
840	17	7.6 160145	9	AL161612	Human DNA	913	17	7.6 164263	9	AC007497	AC007497	Homo sapi
841	17	7.6 160197	9	AP004221	Homo sapi	914	17	7.6 164272	9	AC073657	AC073657	Homo sapi
842	17	7.6 160199	9	AF391285	Homo sapi	915	17	7.6 164461	9	AC083806	AC083806	Homo sapi
843	17	7.6 160254	2	AC007763	Homo sapi	916	17	7.6 164479	9	AC103922	AC103922	Homo sapi
844	17	7.6 160275	2	AC013701	Homo sapi	917	17	7.6 164485	2	AC025340	AC025340	Homo sapi
845	17	7.6 160373	2	AC024548	Homo sapi	918	17	7.6 164500	2	AL359698	AL359698	Homo sapi
846	17	7.6 160378	2	AC090076	Homo sapi	919	17	7.6 164508	2	AC104130	AC104130	Homo sapi
847	17	7.6 160445	2	AC022376	Homo sapi	920	17	7.6 164519	9	AL138712	AL138712	Human DNA
848	17	7.6 160601	9	AC021107	Homo sapi	921	17	7.6 164522	9	AC026191	AC026191	Homo sapi
849	17	7.6 160601	9	AC093517	Homo sapi	922	17	7.6 164601	2	AC104476	AC104476	Pan trogl
850	17	7.6 160655	9	AC064874	Homo sapi	923	17	7.6 164632	2	AC025624	AC025624	Homo sapi
851	17	7.6 160655	9	AC064874	Homo sapi	924	17	7.6 164651	2	AC020994	AC020994	Homo sapi
852	17	7.6 160779	2	AC066583	Homo sapi	925	17	7.6 164810	2	AC023411	AC023411	Homo sapi
853	17	7.6 160861	2	AC103586	Homo sapi	926	17	7.6 164840	2	AC011127	AC011127	Homo sapi
854	17	7.6 160864	2	AC021993	Homo sapi	927	17	7.6 164878	2	AP001588	AP001588	Homo sapi
855	17	7.6 160877	2	AC026560	Homo sapi	928	17	7.6 165029	2	AC084278	AC084278	Homo sapi
856	17	7.6 160892	2	AC023910	Homo sapi	929	17	7.6 165287	9	AC090599	AC090599	Homo sapi
857	17	7.6 160903	2	AP002776	Homo sapi	930	17	7.6 165516	9	AC005912	AC005912	Homo sapi
858	17	7.6 160904	2	AC067896	Homo sapi	931	17	7.6 165556	9	AC092295	AC092295	Homo sapi
859	17	7.6 161164	2	AC022278	Homo sapi	932	17	7.6 165617	9	CNS0000K	AL049840	Human chr
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861	17	7.6 161422	2	AC108686	Homo sapi	934	17	7.6 165888	2	AC025555	AC025555	Homo sapi
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863	17	7.6 161445	2	AP000938	Homo sapi	936	17	7.6 166035	2	AC080131	AC080131	Trypanoso
864	17	7.6 161505	9	AP001888	Homo sapi	937	17	7.6 166143	2	AL356960	AL356960	Homo sapi
865	17	7.6 161548	9	AP001929	Homo sapi	938	17	7.6 166178	2	AP002990	AP002990	Homo sapi
866	17	7.6 161586	2	AC079360	Homo sapi	939	17	7.6 166192	9	AC096737	AC096737	Homo sapi
867	17	7.6 161593	9	HSBA49G10	Human DNA	940	17	7.6 166233	2	AC048369	AC048369	Homo sapi
868	17	7.6 161737	9	AC090512	Homo sapi	941	17	7.6 166237	9	AL139379	AL139379	Human DNA
869	17	7.6 161755	2	AC083755	Homo sapi	942	17	7.6 166336	2	AC007716	AC007716	Homo sapi
870	17	7.6 161806	2	AC016495	Homo sapi	943	17	7.6 166396	2	AC023957	AC023957	Homo sapi
871	17	7.6 161900	9	AC096729	Homo sapi	944	17	7.6 166534	2	AC034209	AC034209	Homo sapi
872	17	7.6 161933	2	AL392045	Human DNA	945	17	7.6 166585	2	AC108039	AC108039	Homo sapi
873	17	7.6 161936	2	AC013302	Homo sapi	946	17	7.6 166606	2	AC099562	AC099562	Homo sapi
874	17	7.6 161987	2	AC006070	Homo sapi	947	17	7.6 166664	9	AL353573	AL353573	Human DNA
875	17	7.6 162066	2	AL592295	Homo sapi	948	17	7.6 166731	9	AC093910	AC093910	Homo sapi
876	17	7.6 162150	9	AC093877	Homo sapi	949	17	7.6 166731	9	AC093910	AC093910	Homo sapi

950	17	7.6	166757	2	AC097490	Homo sapi
951	17	7.6	166758	2	AC024428	Homo sapi
952	17	7.6	166857	2	NS01RG5	Homo sapi
953	17	7.6	166970	2	AC094775	Rattus no
954	17	7.6	167022	9	AC010238	Homo sapi
955	17	7.6	167080	9	AC007014	Homo sapi
956	17	7.6	167101	9	AC002094	Genomic s
957	17	7.6	167124	2	AC091559	Homo sapi
958	17	7.6	167292	2	AC068365	Homo sapi
959	17	7.6	167323	6	AX332231	Sequence
960	17	7.6	167343	6	AX335067	Sequence
961	17	7.6	167343	9	HS096629	Human chrom
962	17	7.6	167398	9	CNS07EET	Human chr
963	17	7.6	167429	2	AC099394	Homo sapi
964	17	7.6	167477	9	AL442643	Human DNA
965	17	7.6	167498	2	AP000750	Homo sapi
966	17	7.6	167522	2	AC097004	Papio cyn
967	17	7.6	167563	9	AC069280	Homo sapi
968	17	7.6	167570	9	AC092668	Homo sapi
969	17	7.6	167687	2	AC023476	Homo sapi
970	17	7.6	167863	2	AL590651	Homo sapi
971	17	7.6	167966	2	AC015912	Homo sapi
972	17	7.6	167998	9	AL353662	Human DNA
973	17	7.6	168018	2	AL592186	Homo sapi
974	17	7.6	168140	2	AC008248	Homo sapi
975	17	7.6	168145	9	AL159171	Human DNA
976	17	7.6	168154	2	AC016456	Homo sapi
977	17	7.6	168168	2	AC012283	Homo sapi
978	17	7.6	168258	2	AC018703	Homo sapi
979	17	7.6	168285	9	AC008575	Homo sapi
980	17	7.6	168425	2	AC012198	Homo sapi
981	17	7.6	168468	9	AL450346	Human DNA
982	17	7.6	168468	2	AC011658	Homo sapi
983	17	7.6	168473	2	AC063917	Homo sapi
984	17	7.6	168509	2	AC015570	Homo sapi
985	17	7.6	168648	2	AC096892	Homo sapi
986	17	7.6	168659	2	AL359883	Homo sapi
987	17	7.6	168710	2	AP000894	Homo sapi
988	17	7.6	168710	9	AC021849	Homo sapi
989	17	7.6	168865	2	AC093123	Papio cyn
990	17	7.6	168872	9	AC073325	Homo sapi
991	17	7.6	168887	9	AL662833	Human DNA
992	17	7.6	168897	2	AC025787	Homo sapi
993	17	7.6	168937	2	AC018747	Homo sapi
994	17	7.6	169103	2	AC025687	Homo sapi
995	17	7.6	169118	2	AC096645	Homo sapi
996	17	7.6	169234	9	CNS06C7Q	Human chr
997	17	7.6	169235	2	AC026224	Homo sapi
998	17	7.6	169323	2	AL161906	Homo sapi
999	17	7.6	169370	2	AC022954	Homo sapi
1000	17	7.6	169374	2	AC026050	Homo sapi

ALIGNMENTS

RESULT	1	AR153509	225 bp	DNA	linear	PAT 08-AUG-2001
LOCUS		Sequence 18 from patent US 6235525.				
DEFINITION		Sequence 18 from patent US 6235525.				
ACCESSION		AR153509.1				
VERSION		AR153509.1				
KEYWORDS		GI:15121041				
SOURCE		Unknown.				
ORGANISM		Unknown.				
REFERENCE		1 (bases 1 to 225)				
AUTHORS		van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.				
TITLE		Isolated nucleic acid molecules coding for tumor rejection antigen precursor Mage-3 and uses thereof				
JOURNAL		Patent: US 6235525-A 18 22-MAY-2001;				
FEATURES		Location/Qualifiers				
source		1. .225				

BASE COUNT	44 a	65 c	58 g	58 t		
ORIGIN						
Query Match	100.0%;	Score 225;	DB 6;	Length 225;		
Best Local Similarity	100.0%;	Pred. No. 6.1e-121;				
Matches	225;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	TATTTCTTCTGATCTTCAGCAAGCTTCGATTCCTTGAGCTGGTCTTTGGGATC	60			
Db	1	TATTTCTTCTGATCTTCAGCAAGCTTCGATTCCTTGAGCTGGTCTTTGGGATC	60			
QY	61	GAGCTGATGAAGTGGACCCATCGGCACTGTACATCTTTGCCACCTGCCTGGGCTC	120			
Db	61	GAGCTGATGAAGTGGACCCATCGGCACTGTACATCTTTGCCACCTGCCTGGGCTC	120			
QY	121	TCCTAGATGGCTGCTGGTGCATATCAGATCATGCCAGGACAGGCTTCCTGATAATC	180			
Db	121	TCCTAGATGGCTGCTGGTGCATATCAGATCATGCCAGGACAGGCTTCCTGATAATC	180			
QY	181	ATCTGGCCATATCGCAAGAGGGGCTGTGCCCTGAGGAG	225			
Db	181	ATCTGGCCATATCGCAAGAGGGGCTGTGCCCTGAGGAG	225			
RESULT	2					
LOCUS		I36933	225 bp	DNA	linear	PAT 13-MAY-1997
DEFINITION		Sequence 18 from patent US 5612201.				
ACCESSION		I36933				
VERSION		I36933.1				
KEYWORDS		GI:2084893				
SOURCE		Unknown.				
ORGANISM		Unknown.				
REFERENCE		1 (bases 1 to 225)				
AUTHORS		De Plaen,E., Boon-Falleur,T., Lethe,B., Szikora,J.-P., De Smet,C. and Chomez,P.				
TITLE		Isolated nucleic acid molecules useful in determining expression of a tumor rejection antigen precursor				
JOURNAL		Patent: US 5612201-A 18 18-MAR-1997;				
FEATURES		Location/Qualifiers				
source		1. .225				
BASE COUNT	44 a	65 c	58 g	58 t		
ORIGIN						
Query Match	100.0%;	Score 225;	DB 6;	Length 225;		
Best Local Similarity	100.0%;	Pred. No. 6.1e-121;				
Matches	225;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	TATTTCTTCTGATCTTCAGCAAGCTTCGATTCCTTGAGCTGGTCTTTGGGATC	60			
Db	1	TATTTCTTCTGATCTTCAGCAAGCTTCGATTCCTTGAGCTGGTCTTTGGGATC	60			
QY	61	GAGCTGATGAAGTGGACCCATCGGCACTGTACATCTTTGCCACCTGCCTGGGCTC	120			
Db	61	GAGCTGATGAAGTGGACCCATCGGCACTGTACATCTTTGCCACCTGCCTGGGCTC	120			
QY	121	TCCTAGATGGCTGCTGGTGCATATCAGATCATGCCAGGACAGGCTTCCTGATAATC	180			
Db	121	TCCTAGATGGCTGCTGGTGCATATCAGATCATGCCAGGACAGGCTTCCTGATAATC	180			
QY	181	ATCTGGCCATATCGCAAGAGGGGCTGTGCCCTGAGGAG	225			
Db	181	ATCTGGCCATATCGCAAGAGGGGCTGTGCCCTGAGGAG	225			
RESULT	3					
LOCUS		AR167371	945 bp	DNA	linear	PAT 17-DEC-2001

DEFINITION Sequence 7 from patent US 6287569.

ACCESSION AR167371

VERSION AR167371.1 GI:17903147

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 945)

AUTHORS Kipps,T.J. and Wu,Y.

TITLE Vaccines with enhanced intracellular processing

JOURNAL Patent: US 6287569-A 11-SEP-2001;

FEATURES Location/Qualifiers

source 1..945

BASE COUNT 213 a 254 c 275 g 203 t

ORIGIN

Query Match 69.8%; Score 157; DB 6; Length 945;

Best Local Similarity 100.0%; Pred. No. 6.3e-81;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATCGAG 63

Db 436 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATCGAG 495

QY 64 CTGATGGAAGTGGACCCCATCGCCACGTGTACATCTTTGCCACCTGGGCGCTCTCC 123

Db 496 CTGATGGAAGTGGACCCCATCGCCACGTGTACATCTTTGCCACCTGGGCGCTCTCC 555

QY 124 TAGCATGGCCTGCTGGTGACATCAGATCATGCCCA 160

Db 556 TAGCATGGCCTGCTGGTGACATCAGATCATGCCCA 592

RESULT 4

HSU10339

LOCUS HSU10339 945 bp mRNA linear PRI 13-JUN-1994

DEFINITION Human MAGE-3b mRNA, complete cds.

ACCESSION U10339

VERSION U10339.1 GI:499121

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 945)

AUTHORS Fenton,R.G.

TITLE Cloning and Analysis of MAGE-1 Related Genes

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 945)

AUTHORS Fenton,R.G.

TITLE Direct Submission

JOURNAL Submitted (03-JUN-1994) Robert G. Fenton, BRMP, NCI-FCRDC,

Frederick, MD 21702, USA

FEATURES Location/Qualifiers

source 1..945

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="MAGE-3b"

/haplotype="HLA-A1/A2"

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/clone\_lib="DM150 library"

/dev\_stage="adult"

/note="Cancer patient"

1..945

/codon\_start=1

/product="MAGE-3b"

/protein\_id="AA119006.1"

/db\_xref="GI:499122"

/translation="MPLEQRQHCKPERGLEARGALGLVGAQAPATEEQEAASSST

CDS

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SEFQAALSRKVKAKLHFLLLKYRAREPVTYKAEMLGSGVGNWQIFFPFVIFSKASDQL  
VFGIELMEVDPIGHVYIFATCLGLSYDGLLDNIMPKTGFLIILAIKAGDCAPE  
EKIWEELSVLEFEGREDSIFGDPKKLLTQYFQENYLEYRQVPGSDPACYEFLMGPR  
ALIIETSYVKVLHVMKISGGPRISYPLLLHEWALREGEE"

BASE COUNT 213 a 254 c 275 g 203 t

ORIGIN

Query Match 69.8%; Score 157; DB 9; Length 945;

Best Local Similarity 100.0%; Pred. No. 6.3e-81;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATCGAG 63

Db 436 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATCGAG 495

QY 64 CTGATGGAAGTGGACCCCATCGCCACGTGTACATCTTTGCCACCTGGGCGCTCTCC 123

Db 496 CTGATGGAAGTGGACCCCATCGCCACGTGTACATCTTTGCCACCTGGGCGCTCTCC 555

QY 124 TAGCATGGCCTGCTGGTGACATCAGATCATGCCCA 160

Db 556 TAGCATGGCCTGCTGGTGACATCAGATCATGCCCA 592

RESULT 5

AR167377

LOCUS AR167377 1019 bp DNA linear PAT 17-DEC-2001

DEFINITION Sequence 13 from patent US 6287569.

ACCESSION AR167377

VERSION AR167377.1 GI:17903153

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1019)

AUTHORS Kipps,T.J. and Wu,Y.

TITLE Vaccines with enhanced intracellular processing

JOURNAL Patent: US 6287569-A 13 11-SEP-2001;

FEATURES Location/Qualifiers

source 1..1019

BASE COUNT 224 a 284 c 292 g 219 t

ORIGIN

Query Match 69.8%; Score 157; DB 6; Length 1019;

Best Local Similarity 100.0%; Pred. No. 6.3e-81;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATCGAG 63

Db 501 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATCGAG 560

QY 64 CTGATGGAAGTGGACCCCATCGCCACGTGTACATCTTTGCCACCTGGGCGCTCTCC 123

Db 561 CTGATGGAAGTGGACCCCATCGCCACGTGTACATCTTTGCCACCTGGGCGCTCTCC 620

QY 124 TAGCATGGCCTGCTGGTGACATCAGATCATGCCCA 160

Db 621 TAGCATGGCCTGCTGGTGACATCAGATCATGCCCA 657

RESULT 6

HUMMAGEB

LOCUS HUMMAGEB 1019 bp mRNA linear PRI 07-FEB-1999

DEFINITION Human mRNA for MAGE-6 protein, complete cds.

ACCESSION D32076

VERSION D32076.1 GI:1125015

KEYWORDS MAGE-6 protein; melanoma antigen.

SOURCE Homo sapiens cell-line M73 CDNA to mRNA.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1019)

AUTHORS Imai,Y.

TITLE Direct Submission

JOURNAL Submitted (08-JUL-1994) Yasuhisa Imai, Kurume University School of Medicine, Immunology; Asahi 67, Kurume, Fukuoka 830, Japan

REFERENCE 2 (bases 1 to 1019)

AUTHORS Imai,Y., Shichijo,S., Yamada,A., Katayama,T., Yano,H. and Itoh,K.

TITLE Sequence analysis of the MAGE gene family encoding human tumor-rejection antigens

JOURNAL Gene 160 (2), 287-290 (1995)

MEDLINE 95369706

FEATURES

source

1..1019

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/cell\_line="M73"

66..1010

/standard\_name="melanoma antigen-6"

/note="Nomenclature of MAGE-6 was according to MAGE gene's 27 nucleotide sequences of HLA-A1 binding motif (Traversari et al., 1992)"

/codon\_start=1

/evidence-experimental

/product="MAGE-6 protein"

/protein\_id="BAA06842.1"

/db\_xref="GI:1125016"

/translation="MPLEQRSHCKPEGLRGALGLVGAQAPATERDEAASSST LVEVTIGVPAESDPQSGASLPTTMYPLMSQYEDSSNOEEGPTFPDLE SFQALSRKAKLVHFLLLKYRAREPTVKAEMLGSVGNWQYFFVIFSKASDLSL EKIEWELSVLEVEGEDSIFGDKLLQYFQENYEVYRQVPGSDPACYEFLWGP ALIETSYVKLVHMKISGPRISPLLEHWAAREGE"

BASE COUNT 224 a 284 c 292 g 219 t

ORIGIN

Query Match 69.8%; Score 157; DB 9; Length 1019;

Best Local Similarity 100.0%; Pred. No. 6.3e-81;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTCTCTGTATCTTCAGCAAGCTTCGATTCCTTCAGCTGTGCTTTGGCATCGAG 63

Db 501 TTCTTCTCTGTATCTTCAGCAAGCTTCGATTCCTTCAGCTGTGCTTTGGCATCGAG 560

QY 64 CTGATGGAAGTGGACCCATCGCCAGCTGTACATCTTTGCCACCTGCTGGGCTCTCC 123

Db 561 CTGATGGAAGTGGACCCATCGCCAGCTGTACATCTTTGCCACCTGCTGGGCTCTCC 620

QY 124 TAGATGGCTGCTGGGTGACAATCAGATCATGCCCA 160

Db 621 TAGATGGCTGCTGGGTGACAATCAGATCATGCCCA 657

RESULT 7

AX019384

LOCUS AX019384 1362 bp DNA linear PAT 07-SEP-2000

DEFINITION Sequence 10 from Patent WO9940188.

ACCESSION AX019384

VERSION AX019384.1 GI:10043354

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1362)

AUTHORS Tlaoui,M.M., Cohen,J., Cabazon,S.T. and Vinals,B.C.

TITLE Tumor-associated antigen derivatives from the mage family, and nucleic acid sequences encoding them, used for the preparation of fusion proteins and of compositions for vaccination

JOURNAL Patent: WO 9940188-A 10 12-AUG-1999;

SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)

FEATURES

source

1..1362

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/note="Melanoma tissue"

BASE COUNT 345 a 348 c 383 g 286 t

ORIGIN

Query Match 69.8%; Score 157; DB 6; Length 1362;

Best Local Similarity 100.0%; Pred. No. 6.3e-81;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTCTCTGTATCTTCAGCAAGCTTCGATTCCTTCAGCTGTGCTTTGGCATCGAG 63

Db 826 TTCTTCTCTGTATCTTCAGCAAGCTTCGATTCCTTCAGCTGTGCTTTGGCATCGAG 885

QY 64 CTGATGGAAGTGGACCCATCGCCAGCTGTACATCTTTGCCACCTGCTGGGCTCTCC 123

Db 886 CTGATGGAAGTGGACCCATCGCCAGCTGTACATCTTTGCCACCTGCTGGGCTCTCC 945

QY 124 TAGATGGCTGCTGGGTGACAATCAGATCATGCCCA 160

Db 946 TAGATGGCTGCTGGGTGACAATCAGATCATGCCCA 982

RESULT 8

HSU10691

LOCUS Human MAGE-6 antigen (MAGE6) gene, complete cds.

DEFINITION U10691

ACCESSION U10691.1 GI:533522

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3871)

AUTHORS De Plaen,E., Arden,K., Traversari,C., Gaforio,J.J., Szikora,J.P., De Smet,C., Brasseur,F., van der Bruggen,P., Lethe,B., Lurquin,C., Brasseur,R., Chomez,P., De Backer,O., Cavenee,W. and Boon,T.

TITLE Structure, chromosomal localization, and expression of 12 genes of the MAGE family

JOURNAL Immunogenetics 40 (5), 360-369 (1994)

MEDLINE 95012457

REFERENCE 2 (bases 1 to 3871)

AUTHORS De Plaen,E.

TITLE Direct Submission

JOURNAL Submitted (14-JUN-1994) Etienne De Plaen, Ludwig Institute for Cancer Research, 74 Avenue Hippocrate, Brussels, 1200, Belgium

FEATURES

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/isolate="patient M22"

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QY 64 CTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCCTCTCC 123
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Db 2759 CTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCCTCTCC 2818
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RESULT 9
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DEFINITION Homo sapiens chromosome X map Xq28, complete sequence.
ACCESSION      AF002997
VERSION      AF002997.2 GI:13621226
KEYWORDS      HTG; HTGS_ACTIVEIN.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 245077)
AUTHORS      Galoczy,P., Schilhabel,M., Rosenthal,A. and Platzzer,M.
TITLE      Chromosome X genomic sequence
JOURNAL      Unpublished
REFERENCE      3 (bases 1 to 245077)
AUTHORS      Gloeckner,G., Rosenthal,A., Drescher,B. and Schattevoy,R.
TITLE      Direct Submission
JOURNAL      Submitted (07-MAY-1997) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
REFERENCE      4 (bases 1 to 245077)
AUTHORS      Platzzer,M.
TITLE      Direct Submission
JOURNAL      Submitted (13-APR-2001) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
COMMENT      On Apr 13, 2001 this sequence version replaced gi.4409798.
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42555..245077
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Db 164183 CTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCCTCTCC 164242
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QY 124 TAGCATGGCTCTCTGGTGACAAATCAGATCATGCCA 160
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Db 164243 TAGCATGGCTCTCTGGTGACAAATCAGATCATGCCA 164279
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RESULT 10
LOCUS      AX019380      1212 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 6 from Patent WO9940188.
ACCESSION      AX019380
VERSION      AX019380.1 GI:10043352
KEYWORDS      human.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1212)
AUTHORS      Slaoui,M.M., Cohen,J., Cabezon,S.T. and Vinals,B.C.
TITLE      Tumor-associated antigen derivatives from the mage family, and
nucleic acid sequences encoding them, used for the preparation of
fusion proteins and of compositions for vaccination
JOURNAL      Patent: WO 9940188-A 6 12-AUG-1999;
SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)
FEATURES
source      1..1212
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             /db_xref="taxon:9606"
             /note="Melanoma tissue"
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Best Local Similarity 99.2%; Pred. No. 4.1e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 156 GCCCA 160
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Db 828 GCCCA 832

RESULT 11
AX019376
LOCUS AX019376 1353 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 2 from Patent WO9940188.
ACCESSION AX019376
VERSION AX019376.1 GI:10043350
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 1353)
JOURNAL Slaoui.M.M., Cohen.J., Cabezon.S.T. and Vinals.B.C.
FEATURES Tumor-associated antigen derivatives from the mage family, and
source nucleic acid sequences encoding them, used for the preparation of
fusion proteins and of compositions for vaccination
BASE COUNT SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
ORIGIN JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)
/organism="Homo sapiens"
/db_xref="taxon:9606"
/notes="Melanoma tissue"
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Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 96 CATCTTTGCCACCTGCTGGGCTCTCCCTACGATGGCTGGTGGTGACAATCAGATCAT 155
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QY 156 GCCCA 160
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Db 969 GCCCA 973

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AX343855
LOCUS AX343855 1569 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 1 from Patent WO200892.
ACCESSION AX343855
VERSION AX343855.1 GI:18491925
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (sites)
AUTHORS cabezon Silva,T.E. and Delisse,A.M.
TITLE Triple fusion proteins comprising ubiquitin fused between
JOURNAL thiodoxin and a polypeptide of interest
Patent: WO 0200892-A 1 03-JAN-2002;
SmithKline Beecham Biologics SA (BE)
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Best Local Similarity 99.2%; Pred. No. 4.2e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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ACCESSION AR153502
VERSION AR153502.1 GI:15121034
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1640)
AUTHORS van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.
TITLE Isolated nucleic acid molecules coding for tumor rejection antigen
JOURNAL precursor MAGE-3 and uses thereof
FEATURES Patent: US 6235525-A 11 22-MAY-2001;
Location/Qualifiers
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QY 156 GCCCA 160
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Db 759 GCCCA 763

RESULT 14
I36926
LOCUS I36926 1640 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 11 from patent US 5612201.
ACCESSION I36926
VERSION I36926.1 GI:2084886
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1640)
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AUTHORS De Plaen, E., Boon-Palleur, T., Lethe, B., Szikora, J.-P., De Smet, C. and Chomez, P.  
TITLE Isolated nucleic acid molecules useful in determining expression of a tumor rejection antigen precursor  
JOURNAL Patent: US 5612201-A 11 18-MAR-1997;  
FEATURES Location/Qualifiers  
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QY 156 GCCCA 160  
Db 759 GCCCA 763  
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BC011744 1663 bp mRNA linear PRI 02-AUG-2001  
LOCUS  
DEFINITION Homo sapiens, Similar to melanoma antigen, family A, 3, clone  
MGC:19667 IMAGE:3345801, mRNA, complete cds.  
ACCESSION BC011744  
VERSION BC011744.1 GI:15079897  
KEYWORDS MGC.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1663)  
Strausberg, R.  
Direct Submission  
Submitted (30-JUL-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabbs-re@mail.nih.gov](mailto:cgabbs-re@mail.nih.gov)  
Tissue Procurement: ATCC/DCTD/DTP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,  
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,  
Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,  
Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,  
Zhang, L.-H. and Green, E.D.  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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FEATURES  
source

Location/Qualifiers  
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Copyright (c) 1993 - 2000 CompuGen Ltd.

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#### SUMMARIES

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3	225	100.0	225	20	AAQ84122
4	174	77.3	225	16	AAQ01166
5	157	69.8	1362	20	AAQ87596
6	157	69.8	1375	19	AAV22716
7	157	69.8	4204	22	AAQ02056
8	74	32.9	666	22	AAD18141
9	74	32.9	945	22	AAD12993

Haemagglutinin-MAG	10	74	32.9	1212	20	AAQ87592	Haemagglutinin-MAG
Lipoprotein D-MAGE	11	74	32.9	1353	20	AAQ87588	Lipoprotein D-MAGE
Tumour rejection a	12	74	32.9	1640	15	AAQ72480	Tumour rejection a
MAGE-3 gene. Homo	13	74	32.9	1640	20	AAQ84116	MAGE-3 gene. Homo
cDNA encoding MAGE	14	74	32.9	4204	20	AAQ26974	cDNA encoding MAGE
Human MAGE-A3 nucl	15	74	32.9	4204	21	AAA37927	Human MAGE-A3 nucl
Human melanoma ass	16	74	32.9	4204	22	AAD18140	Human melanoma ass
Human MAGE-3 DNA.	17	69	30.7	379	18	AAT63345	Human MAGE-3 DNA.
MAGE-3 CDNA. Homo	18	69	30.7	1640	13	AAQ32355	MAGE-3 CDNA. Homo
Baboon MAGE-3 homo	19	56	24.9	268	18	AAT63347	Baboon MAGE-3 homo
Baboon MAGE-3 homo	20	56	24.9	376	18	AAT63346	Baboon MAGE-3 homo
Baboon MAGE-3 homo	21	49	21.8	271	18	AAT63350	Baboon MAGE-3 homo
Baboon MAGE-3 homo	22	49	21.8	378	18	AAT63349	Baboon MAGE-3 homo
Baboon MAGE-3 homo	23	43	19.1	271	18	AAT63348	Baboon MAGE-3 homo
Human MAGE-12 cDNA	24	36	16.0	727	22	AAD21285	Human MAGE-12 cDNA
Probe #14830 for g	25	36	16.0	920	22	ABA36364	Probe #14830 for g
Probe #14233 for g	26	36	16.0	920	22	AAI24300	Probe #14233 for g
Probe #18262 used	27	36	16.0	920	22	AAI49576	Probe #18262 used
Probe #4953 for ge	28	36	16.0	1956	22	ABA26487	Probe #4953 for ge
Probe #5051 for ge	29	36	16.0	1956	22	AAI15118	Probe #5051 for ge
Probe #5139 used t	30	36	16.0	1956	22	AAI36453	Probe #5139 used t
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Tumour rejection a	32	36	16.0	4157	15	AAQ72478	Tumour rejection a
MAGE-2 gene. Homo	33	36	16.0	4157	20	AAQ84114	MAGE-2 gene. Homo
MAGE-6 nonapeptide	34	27	12.0	27	15	AAQ44759	MAGE-6 nonapeptide
MAGE-3 gene specif	35	27	12.0	27	17	AAT35415	MAGE-3 gene specif
Human MAGE-12 gene	36	26	11.6	26	20	AAZ28066	Human MAGE-12 gene
Human MAGE-12 gene	37	26	11.6	1030	22	AAD21286	Human MAGE-12 gene
Human MAGE-12 gene	38	26	11.6	4523	22	AAD06131	Human MAGE-12 gene
MAGE-6 PCR primer	39	24	10.7	24	16	AAQ05065	MAGE-6 PCR primer
Antisense PCR prim	40	24	10.7	24	21	AAZ35541	Antisense PCR prim
MAGE-A6 antisense	41	24	10.7	24	22	AAF84241	MAGE-A6 antisense
MAGE tumour reject	42	24	10.7	24	22	AAQ67098	MAGE tumour reject
MAGE 6 gene captur	43	24	10.7	27	24	ABA81874	MAGE 6 gene captur
cDNA encoding MAGE	44	24	10.7	44	18	AAQ06033	cDNA encoding MAGE
Upstream primer fo	45	23	10.2	31	21	AAQ09232	Upstream primer fo
Human MAGE-A1 mini	46	23	10.2	72	22	AAD12990	Human MAGE-A1 mini
cDNA encoding MAGE	47	23	10.2	126	18	AAQ06032	cDNA encoding MAGE
ALVAC(1)-MAGE-1/3	48	23	10.2	141	24	AAI67603	ALVAC(1)-MAGE-1/3
Human MAGE-A1 cDNA	49	23	10.2	313	24	AAI67604	Human MAGE-A1 cDNA
H6/MAGE-1 expressi	50	23	10.2	930	22	AAQ12987	H6/MAGE-1 expressi
H6/MAGE-1 expressi	51	23	10.2	1084	15	AAQ67866	H6/MAGE-1 expressi
H6/MAGE-1 expressi	52	23	10.2	1084	20	AAQ08442	H6/MAGE-1 expressi
H6/MAGE-1 expressi	53	23	10.2	1094	15	AAQ67865	H6/MAGE-1 expressi
CLYTA-MAGE-1-His f	54	23	10.2	1094	20	AAQ08441	CLYTA-MAGE-1-His f
Lipoprotein D-MAGE	55	23	10.2	1338	20	AAQ87593	Lipoprotein D-MAGE
Nucleotide sequenc	56	23	10.2	1341	20	AAQ87591	Nucleotide sequenc
Tumour rejection a	57	23	10.2	1624	22	AAQ24676	Tumour rejection a
cDNA encoding huma	58	23	10.2	1691	20	AAQ69719	cDNA encoding huma
MAGE-5 CDNA. Homo	59	23	10.2	1916	21	AAQ64632	MAGE-5 CDNA. Homo
Tumour rejection a	60	23	10.2	2226	13	AAQ32360	Tumour rejection a
MAGE-5 coding sequ	61	23	10.2	2226	15	AAQ72485	MAGE-5 coding sequ
MAGE-51 genomic DN	62	23	10.2	2226	20	AAQ84104	MAGE-51 genomic DN
Tumour rejection a	63	23	10.2	2305	13	AAQ32361	Tumour rejection a
MAGE-51 gene. Hom	64	23	10.2	2305	16	AAQ72486	MAGE-51 gene. Hom
MAGE-51 gene. Hom	65	23	10.2	2305	15	AAQ01165	MAGE-51 gene. Hom
E antigen precursor	66	23	10.2	2305	20	AAQ84121	E antigen precursor
Antigen E gene. H	67	23	10.2	2418	20	AAQ84103	Antigen E gene. H
Tumour rejection a	68	23	10.2	2419	13	AAQ32351	Tumour rejection a
M2-MEL antigen E	69	23	10.2	2419	15	AAQ72476	M2-MEL antigen E
Antigen E coding s	70	23	10.2	2419	16	AAQ05086	Antigen E coding s
Tumour rejection a	71	23	10.2	2420	15	AAQ84112	Tumour rejection a
Human melanoma ant	72	23	10.2	2420	16	AAQ72472	Human melanoma ant
MAGE-1 nucleic aci	73	23	10.2	2420	13	AAQ85435	MAGE-1 nucleic aci
Tumour rejection a	74	23	10.2	5674	15	AAQ32352	Tumour rejection a
MAGE-1 gene. Homo	75	23	10.2	5674	15	AAQ72477	MAGE-1 gene. Homo
Tumour rejection a	76	23	10.2	5674	20	AAQ84113	Tumour rejection a
MAGE-3 nonapeptide	77	23	10.2	5724	16	AAQ98902	MAGE-3 nonapeptide
MAGE-3 nonapeptide	78	21	9.3	27	15	AAQ44754	MAGE-3 nonapeptide
MAGE 1/3 DNA fragm	79	21	9.3	27	17	AAQ35411	MAGE 1/3 DNA fragm
Probe #11868 used	80	21	9.3	54	22	AAI67608	Probe #11868 used
cDNA encoding huma	81	21	9.3	563	22	AAI43182	cDNA encoding huma
	82	21	9.3	1765	21	AAA64633	

83	21	1810	13	AAQ32364	MAGE-8 genomic DNA	156	17	7.6	1947	16	AAAT01167	MAGE-7 gene.
84	21	1810	15	AAQ72489	Tumour rejection a	157	17	7.6	1947	20	AAH84123	MAGE-7 gene.
85	21	1810	16	AAQ72489	MAGE-8 gene.	158	17	7.6	2052	22	AAH84527	Capsid protein VP4
86	21	1810	20	AAH84124	MAGE-8 gene.	159	17	7.6	2052	22	AAH84527	Zea mays DNA fragm
87	21	1810	21	AAQ01315	Human MAGE-A8 part	160	17	7.6	2052	21	AAH84478	Human polynucleoti
88	21	1810	21	AAQ01315	Human MAGE-A8 gene	161	17	7.6	2052	22	AAH84478	Human polynucleoti
89	21	1810	21	AAQ01315	MAGE-3 gene forwar	162	17	7.6	2052	22	AAH84478	Human polynucleoti
90	20	1810	20	AAQ01315	Human immune/haema	163	17	7.6	2052	22	AAH84478	CNS disorder-relat
91	20	1810	20	AAQ01315	Human immune/haema	164	17	7.6	2052	22	AAH84478	Human cDNA sequenc
92	19	1810	22	AAQ01315	Human breast cancer	165	17	7.6	2052	22	AAH84478	Human immune/haema
93	19	1810	22	AAQ01315	Human breast cancer	166	17	7.6	2052	22	AAH84478	Human immune/haema
94	19	1810	22	AAQ01315	Human breast cancer	167	17	7.6	2052	22	AAH84478	Genomic sequence #
95	19	1810	22	AAQ01315	Human breast cancer	168	17	7.6	2052	22	AAH84478	Human immune/haema
96	19	1810	22	AAQ01315	Human breast cancer	169	17	7.6	2052	22	AAH84478	Genomic sequence #
97	19	1810	22	AAQ01315	Human breast cancer	170	17	7.6	2052	22	AAH84478	Human immune/haema
98	19	1810	22	AAQ01315	Human breast cancer	171	17	7.6	2052	22	AAH84478	Genomic sequence #
99	18	1810	22	AAQ01315	Human breast cancer	172	17	7.6	2052	22	AAH84478	Genomic sequence #
100	18	1810	22	AAQ01315	Human breast cancer	173	17	7.6	2052	22	AAH84478	Human immune/haema
101	18	1810	22	AAQ01315	Human breast cancer	174	17	7.6	2052	22	AAH84478	Human immune/haema
102	18	1810	22	AAQ01315	Human breast cancer	175	17	7.6	2052	22	AAH84478	Genomic sequence #
103	18	1810	22	AAQ01315	Human breast cancer	176	17	7.6	2052	22	AAH84478	Human immune/haema
104	18	1810	22	AAQ01315	Human breast cancer	177	17	7.6	2052	22	AAH84478	Genomic sequence #
105	18	1810	22	AAQ01315	Human breast cancer	178	17	7.6	2052	22	AAH84478	Genomic sequence #
106	18	1810	22	AAQ01315	Human breast cancer	179	17	7.6	2052	22	AAH84478	Human immune/haema
107	18	1810	22	AAQ01315	Human breast cancer	180	17	7.6	2052	22	AAH84478	Human immune/haema
108	18	1810	22	AAQ01315	Human breast cancer	181	17	7.6	2052	22	AAH84478	Human yes1 gene.
109	18	1810	22	AAQ01315	Human breast cancer	182	17	7.6	2052	22	AAH84478	Sequence of a synt
110	18	1810	22	AAQ01315	Human breast cancer	183	17	7.6	2052	22	AAH84478	Human foetal liver
111	18	1810	22	AAQ01315	Human breast cancer	184	17	7.6	2052	22	AAH84478	Probe #16546 for g
112	18	1810	22	AAQ01315	Human breast cancer	185	17	7.6	2052	22	AAH84478	Human brain expres
113	18	1810	22	AAQ01315	Human breast cancer	186	17	7.6	2052	22	AAH84478	Human bone marrow
114	18	1810	22	AAQ01315	Human breast cancer	187	17	7.6	2052	22	AAH84478	Probe #15661 for g
115	18	1810	22	AAQ01315	Human breast cancer	188	17	7.6	2052	22	AAH84478	Probe #21271 used
116	18	1810	22	AAQ01315	Human breast cancer	189	17	7.6	2052	22	AAH84478	Human genome fragm
117	18	1810	22	AAQ01315	Human breast cancer	190	17	7.6	2052	22	AAH84478	Human secreted exp
118	18	1810	22	AAQ01315	Human breast cancer	191	17	7.6	2052	22	AAH84478	Human secreted po
119	18	1810	22	AAQ01315	Human breast cancer	192	17	7.6	2052	22	AAH84478	Human biallelic po
120	18	1810	22	AAQ01315	Human breast cancer	193	17	7.6	2052	22	AAH84478	Human foetal liver
121	17	7.6	72	24	AAH84478	194	16	7.1	251	251	AAH84478	Human bone marrow
122	17	7.6	106	22	AAH84478	195	16	7.1	251	251	AAH84478	3' nucleotide port
123	17	7.6	131	21	AAH84478	196	16	7.1	251	251	AAH84478	Human secreted pro
124	17	7.6	134	21	AAH84478	197	16	7.1	251	251	AAH84478	Human gene expres
125	17	7.6	241	22	AAH84478	198	16	7.1	251	251	AAH84478	Human single nucle
126	17	7.6	339	22	AAH84478	199	16	7.1	251	251	AAH84478	Human single nucle
127	17	7.6	345	20	AAH84478	200	16	7.1	251	251	AAH84478	DNA encoding novel
128	17	7.6	394	22	AAH84478	201	16	7.1	251	251	AAH84478	Novel human polynu
129	17	7.6	396	22	AAH84478	202	16	7.1	251	251	AAH84478	Novel human polynu
130	17	7.6	401	22	AAH84478	203	16	7.1	251	251	AAH84478	Human foetal liver
131	17	7.6	401	22	AAH84478	204	16	7.1	251	251	AAH84478	Human foetal liver
132	17	7.6	409	22	AAH84478	205	16	7.1	251	251	AAH84478	Probe #4163 for ge
133	17	7.6	448	22	AAH84478	206	16	7.1	251	251	AAH84478	Human bone marrow
134	17	7.6	451	22	AAH84478	207	16	7.1	251	251	AAH84478	Probe #4135 used t
135	17	7.6	466	21	AAH84478	208	16	7.1	251	251	AAH84478	Human foetal liver
136	17	7.6	504	22	AAH84478	209	16	7.1	251	251	AAH84478	Probe #14063 for g
137	17	7.6	539	22	AAH84478	210	16	7.1	251	251	AAH84478	Human bone marrow
138	17	7.6	539	22	AAH84478	211	16	7.1	251	251	AAH84478	Probe #9130 used t
139	17	7.6	539	22	AAH84478	212	16	7.1	251	251	AAH84478	Human foetal liver
140	17	7.6	539	22	AAH84478	213	16	7.1	251	251	AAH84478	Human renal cancer
141	17	7.6	539	22	AAH84478	214	16	7.1	251	251	AAH84478	Human bone marrow
142	17	7.6	539	22	AAH84478	215	16	7.1	251	251	AAH84478	Human foetal liver
143	17	7.6	539	22	AAH84478	216	16	7.1	251	251	AAH84478	Probe #6666 for ge
144	17	7.6	539	22	AAH84478	217	16	7.1	251	251	AAH84478	Human brain expres
145	17	7.6	539	22	AAH84478	218	16	7.1	251	251	AAH84478	Human bone marrow
146	17	7.6	539	22	AAH84478	219	16	7.1	251	251	AAH84478	Probe #6464 for ge
147	17	7.6	539	22	AAH84478	220	16	7.1	251	251	AAH84478	Probe #1819 used t
148	17	7.6	539	22	AAH84478	221	16	7.1	251	251	AAH84478	Human colon cancer
149	17	7.6	539	22	AAH84478	222	16	7.1	251	251	AAH84478	DNA encoding novel
150	17	7.6	539	22	AAH84478	223	16	7.1	251	251	AAH84478	DNA encoding novel
151	17	7.6	539	22	AAH84478	224	16	7.1	251	251	AAH84478	Human colon cancer
152	17	7.6	539	22	AAH84478	225	16	7.1	251	251	AAH84478	Human immune/haema
153	17	7.6	539	22	AAH84478	226	16	7.1	251	251	AAH84478	Human DNA polymera
154	17	7.6	539	22	AAH84478	227	16	7.1	251	251	AAH84478	Human immune/haema
155	17	7.6	539	22	AAH84478	228	16	7.1	251	251	AAH84478	Human immune/haema

c 229	16	7.1	805	22	AAI97504	Human neuroblastom	302	16	7.1	6029	22	AAF81680	Pseudomonas polyes
c 230	16	7.1	837	22	AAH31595	Human olfactory re	303	16	7.1	6151	16	AAQ59961	Human excitatory a
c 231	16	7.1	916	22	AAH99352	Human protein enco	304	16	7.1	6260	19	AAV52729	Human hepatocyte n
c 232	16	7.1	952	22	AAH32030	Human olfactory re	305	16	7.1	7146	19	AAV38933	Nucleic acid seque
c 233	16	7.1	961	21	AAA09237	MAGE-A4 open readi	c 306	16	7.1	8140	22	ABA20556	Human nervous syst
c 234	16	7.1	1022	20	AAH40199	MAGE-4 encoding ge	307	16	7.1	8165	22	AAK82672	Human immune/haema
c 235	16	7.1	1068	13	AAQ32359	MAGE-4 cDNA. Homo	c 308	16	7.1	8452	22	AAK59864	Human novel cytoki
c 236	16	7.1	1068	15	AAQ72484	Tumour rejection a	c 309	16	7.1	8580	24	AAK59864	Human novel cytoki
c 237	16	7.1	1068	20	AAH4120	MAGE-4 gene. Homo	c 310	16	7.1	8734	22	ABA09012	Arabidopsis DM74 (
c 238	16	7.1	1141	21	AAH47407	Arabidopsis thalia	c 311	16	7.1	8734	22	AAI59594	Human TRAP240 homo
c 239	16	7.1	1175	21	AAH38066	Arabidopsis thalia	c 312	16	7.1	8761	22	AAI57808	Human polynucleoti
c 240	16	7.1	1320	21	AAH38937	Human pancreatic c	c 313	16	7.1	8761	22	AAI57808	Human polynucleoti
c 241	16	7.1	1370	22	AAI61145	Human polynucleoti	c 314	16	7.1	8785	23	AAK85661	DNA encoding novel
c 242	16	7.1	1412	13	AAQ32365	MAGE-9 genomic DNA	c 315	16	7.1	11742	22	ABA20557	Human nervous syst
c 243	16	7.1	1412	15	AAQ72490	Tumour rejection a	c 316	16	7.1	11742	22	AAK75069	Human immune/haema
c 244	16	7.1	1412	16	AAH01169	MAGE-9 gene. Homo	c 317	16	7.1	12468	22	AAK67330	Human immune/haema
c 245	16	7.1	1412	20	AAH84125	MAGE-9 gene. Homo	c 318	16	7.1	13419	23	ABL06569	Drosophila melanog
c 246	16	7.1	1553	24	ABA04479	Human PP712 protei	c 319	16	7.1	14040	22	ABA08209	Human ovarian and
c 247	16	7.1	1603	22	AAH05992	Human DNA modifia	c 320	16	7.1	14040	22	AAI02790	Human reproductive
c 248	16	7.1	1612	21	AAH38992	Arabidopsis thalia	c 321	16	7.1	14040	22	AAI07517	Human reproductiv
c 249	16	7.1	1680	22	AAH81678	Pseudomonas polyes	c 322	16	7.1	19401	23	ABL06568	Drosophila melanog
c 250	16	7.1	1680	22	AAH75376	Pseudomonas sp. st	c 323	16	7.1	19596	22	AAK73967	Human immune/haema
c 251	16	7.1	1692	22	AAH09674	Human bone marrow	c 324	16	7.1	19596	22	AAK73968	Human immune/haema
c 252	16	7.1	1765	21	AAA64633	MAGE-8 genomic DNA	c 325	16	7.1	25002	19	AAV52181	Streptococcus pneu
c 253	16	7.1	1810	13	AAQ32364	MAGE-8 genomic DNA	c 326	16	7.1	25002	19	AAV52181	Human musculoskele
c 254	16	7.1	1810	15	AAQ72489	Tumour rejection a	c 327	16	7.1	26995	22	AAK29963	Human lung antigen
c 255	16	7.1	1810	16	AAH01168	MAGE-8 gene. Homo	c 328	16	7.1	26995	22	AAK29963	Human reproductive
c 256	16	7.1	1810	20	AAH84124	MAGE-8 gene. Homo	c 329	16	7.1	29163	22	AAI05121	Drosophila melanog
c 257	16	7.1	1810	21	AAH01169	MAGE-8 gene. Homo	c 330	15	6.7	31969	23	ABL07768	Human STP2 gene pr
c 258	16	7.1	1810	22	AAH030528	DNA encoding novel	c 331	15	6.7	51	22	AAI77770	Human silent SNP c
c 259	16	7.1	1810	22	AAH030528	Human reproductive	c 332	15	6.7	51	22	AAI77771	Human silent SNP c
c 260	16	7.1	1822	20	AAH22132	Human secreted pro	c 333	15	6.7	51	22	AAI77772	Human silent SNP c
c 261	16	7.1	1826	20	AAH34003	Pseudomonas specie	c 334	15	6.7	51	22	AAI77773	HIV-2 ROD isolate
c 262	16	7.1	1831	21	AAA64634	DNA encoding novel	c 335	15	6.7	57	21	AAK289633	Human breast cance
c 263	16	7.1	1834	22	AAH030527	Human reproductive	c 336	15	6.7	118	22	AAI26303	Human single nucle
c 264	16	7.1	1834	22	AAH030527	Human reproductive	c 337	15	6.7	121	20	AAH86391	Nucleotide sequenc
c 265	16	7.1	1872	20	AAH00622	Human secreted pro	c 338	15	6.7	129	19	AAH41900	Nucleotide sequenc
c 266	16	7.1	2041	20	AAH22118	Human secreted pro	c 339	15	6.7	138	22	AAH41893	Chicken growth hor
c 267	16	7.1	2210	23	ABL05481	Drosophila melanog	c 340	15	6.7	138	22	AAH41893	Nucleotide sequenc
c 268	16	7.1	2306	22	AAH17057	Human cDNA sequenc	c 341	15	6.7	139	22	ABA74725	Human foetal liver
c 269	16	7.1	2306	22	AAH15696	Human cDNA sequenc	c 342	15	6.7	139	22	ABA39436	Probe #17902 for g
c 270	16	7.1	2416	22	AAH99562	Human protein enco	c 343	15	6.7	139	22	AAK49384	Human bone marrow
c 271	16	7.1	2531	13	AAQ32358	MAGE-41 gene. Hom	c 344	15	6.7	139	22	AAI26495	Probe #16428 for g
c 272	16	7.1	2531	13	AAQ32357	MAGE-4 gene. Homo	c 345	15	6.7	272	21	AAI02812	Human secreted pro
c 273	16	7.1	2531	15	AAQ72482	Tumour rejection a	c 346	15	6.7	292	22	ABA71283	Human foetal liver
c 274	16	7.1	2531	15	AAQ72483	Tumour rejection a	c 347	15	6.7	292	22	AAK19585	Human brain expres
c 275	16	7.1	2531	20	AAH84118	MAGE-4 gene. Homo	c 348	15	6.7	292	22	AAK45588	Human bone marrow
c 276	16	7.1	2531	20	AAH84119	MAGE-41 gene. Hom	c 349	15	6.7	292	22	AAI51524	Probe #20210 used
c 277	16	7.1	2678	22	AAH25712	Human DNA polymera	c 350	15	6.7	303	22	ABA16778	Human nervous syst
c 278	16	7.1	2679	22	AAH59359	Human polynucleoti	c 351	15	6.7	306	22	AAI09757	Probe #9748 used t
c 279	16	7.1	2774	15	AAQ66579	Sorbitol dehydroge	c 352	15	6.7	311	22	ABA12049	Human nervous syst
c 280	16	7.1	2899	23	ABL06546	Drosophila melanog	c 353	15	6.7	324	21	AAK29237	Human secreted pro
c 281	16	7.1	3048	23	AAH68823	DNA encoding novel	c 354	15	6.7	328	21	AAK56647	Eucalyptus grandis
c 282	16	7.1	3788	22	AAH16109	Human cDNA sequenc	c 355	15	6.7	345	22	AAK37860	Novel human diagno
c 283	16	7.1	3839	21	AAH01314	Human cDNA sequenc	c 356	15	6.7	346	22	AAI88734	Human polynucleoti
c 284	16	7.1	4206	22	AAH36384	Human cDNA sequenc	c 357	15	6.7	362	22	ABA08365	Human PLA2 homolog
c 285	16	7.1	4272	23	ABL05480	Human cardiovascular	c 358	15	6.7	374	22	AAI86606	Human polynucleoti
c 286	16	7.1	4368	14	AAH049902	Drosophila melanog	c 359	15	6.7	383	22	AAI98945	Human polynucleoti
c 287	16	7.1	4512	24	AAI99832	Glutamic acid rece	c 360	15	6.7	383	22	AAI63295	Human kidney relat
c 288	16	7.1	4790	22	AAI60062	Mouse ischaemic co	c 361	15	6.7	389	20	AAH01140	Human kidney relat
c 289	16	7.1	4808	15	AAQ79375	Human polynucleoti	c 362	15	6.7	389	20	AAH01140	M. tuberculosis an
c 290	16	7.1	4808	15	AAQ79375	Human N-methyl-D-a	c 363	15	6.7	389	22	AAH01140	M. tuberculosis an
c 291	16	7.1	4808	20	AAH28992	Human N-methyl-D-a	c 364	15	6.7	393	21	AAK05312	Mycobacterium tube
c 292	16	7.1	4808	21	AAH28992	Human N-methyl-D-a	c 365	15	6.7	393	21	AAK05312	Human secreted pro
c 293	16	7.1	4808	24	AAH38706	Human NMDAR2A enco	c 366	15	6.7	393	21	AAK05312	Human ORFX ORF1688
c 294	16	7.1	4808	24	AAH38706	Human NMDAR2A enco	c 367	15	6.7	402	22	AAI67166	Novel human polynu
c 295	16	7.1	4858	15	AAH65488	Human NMDA R2a rec	c 368	15	6.7	414	22	AAI67166	Human breast cance
c 296	16	7.1	5092	22	AAH58276	Human polynucleoti	c 369	15	6.7	429	22	AAI04773	Human breast cance
c 297	16	7.1	5418	22	AAH33412	Human polynucleoti	c 370	15	6.7	435	22	AAI04773	Probe #4764 used t
c 298	16	7.1	5418	22	AAH33412	Human polynucleoti	c 371	15	6.7	445	22	ABA3372	Human breast cell
c 299	16	7.1	5571	22	AAH58830	Human polynucleoti	c 372	15	6.7	445	22	ABA3372	Human foetal liver
c 300	16	7.1	5700	23	AAH58830	Human polynucleoti	c 373	15	6.7	445	22	AAK02077	Probe #2030 for ge
c 301	16	7.1	5814	22	AAH52428	DNA encoding novel	c 374	15	6.7	445	22	AAK02077	Human brain expres
c 302	16	7.1	5814	22	AAH52428	Human polynucleoti	c 375	15	6.7	445	22	AAI12110	Probe #2137 used t
c 303	16	7.1	5948	22	AAH52428	Angiotensin conver	c 376	15	6.7	445	22	AAI12110	Probe #2137 used t

375	15	6.7	445	22	AA102031	Probe #2022 used t	c 448	15	6.7	1242	23	ABL21917	Drosophila melanog
376	15	6.7	459	21	AA38179	Arabidopsis thalia	c 449	15	6.7	1266	22	AAH67260	C glutamicum codin
377	15	6.7	462	22	AA08333	Human secreted pro	c 450	15	6.7	1276	22	AA512520	Gene #13 encoding
378	15	6.7	466	22	AA58624	Human foetal liver	c 451	15	6.7	1279	21	AA51790	Wheat farnesyltran
379	15	6.7	466	22	AAK06751	Human brain expres	c 452	15	6.7	1287	22	AAI63858	Human polynucleoti
380	15	6.7	466	22	AAK32462	Human bone marrow	c 453	15	6.7	1294	22	AAI59556	Human polynucleoti
381	15	6.7	466	22	AAI38296	Probe #6982 used t	c 454	15	6.7	1309	22	AAAL01520	Human reproductive
382	15	6.7	470	21	AA57215	Eucalyptus grandis	c 455	15	6.7	1309	22	AAAL01520	Human reproductive
383	15	6.7	508	22	AAAL01474	Human reproductive	c 456	15	6.7	1311	20	AAI63939	Human polynucleoti
384	15	6.7	510	22	AAAL05246	Human colon cancer	c 457	15	6.7	1311	21	AAI63939	Human polynucleoti
385	15	6.7	510	22	AAH35349	Human immune/haema	c 458	15	6.7	1311	22	AAI63939	Human polynucleoti
386	15	6.7	536	22	AAH35349	Human immune/haema	c 459	15	6.7	1311	22	AAI63939	Human polynucleoti
387	15	6.7	541	23	ABLL1369	Drosophila melanog	c 460	15	6.7	1319	22	AAI63939	Human polynucleoti
388	15	6.7	543	22	AAH09833	Human CDNA clone (	c 461	15	6.7	1323	23	ABL07519	Drosophila melanog
389	15	6.7	543	22	AAH09896	Human CDNA clone (	c 462	15	6.7	1338	22	AAI99982	Human FVII encodin
390	15	6.7	556	22	AA526770	Human genomic DNA	c 463	15	6.7	1357	22	AAI99982	Human FVII encodin
391	15	6.7	558	23	AA591397	DNA encoding novel	c 464	15	6.7	1368	22	AAI99982	Human FVII encodin
392	15	6.7	571	22	AAK92505	Human CDNA 3'-end	c 465	15	6.7	1370	21	AAI99982	Human FVII encodin
393	15	6.7	595	22	ABK63027	Human foetal liver	c 466	15	6.7	1386	23	AA591398	Human secreted pro
394	15	6.7	595	22	AAK30287	Probe #8753 for ge	c 467	15	6.7	1401	22	AAH62715	DNA encoding novel
395	15	6.7	595	22	AAK37229	Human bone marrow	c 468	15	6.7	1405	21	AAH62715	Shrimp white spot
396	15	6.7	595	22	AAI18060	Human bone marrow	c 469	15	6.7	1408	21	AAH62715	Arabidopsis thalia
397	15	6.7	612	22	AAK91931	Human CDNA 5'-end	c 470	15	6.7	1461	21	AAH62715	Arabidopsis thalia
398	15	6.7	612	22	AAK93341	Human CDNA clone r	c 471	15	6.7	1463	22	AAH62715	Human protein clon
399	15	6.7	637	22	AAI63864	Human polynucleoti	c 472	15	6.7	1506	24	AA562337	DNA encoding novel
400	15	6.7	650	23	AA577780	DNA encoding novel	c 473	15	6.7	1510	21	AAI15123	Trichoderma reesei
401	15	6.7	687	21	AAAC03777	Human secreted pro	c 474	15	6.7	1516	22	AAI16017	Human CDNA sequenc
402	15	6.7	696	23	AA564851	DNA encoding novel	c 475	15	6.7	1534	23	AA572018	DNA encoding novel
403	15	6.7	701	22	AAK66401	Human immune/haema	c 476	15	6.7	1536	22	AAH76663	Human cell growth
404	15	6.7	735	21	AAAC49868	Human immune/haema	c 477	15	6.7	1541	21	AAH76663	Human secreted pro
405	15	6.7	736	22	AAI97143	Arabidopsis thalia	c 478	15	6.7	1545	22	AAH76663	Human prostate can
406	15	6.7	744	23	AA567339	Human neuroblastom	c 479	15	6.7	1566	23	AAI03693	Drosophila melanog
407	15	6.7	745	22	AA532894	DNA encoding novel	c 480	15	6.7	1570	21	AAI03693	Human ORFX ORF1924
408	15	6.7	745	22	AA532894	Human genomic DNA	c 481	15	6.7	1588	21	AAI03693	Human CDNA sequenc
409	15	6.7	766	21	AAZ97266	Human prostate can	c 482	15	6.7	1592	21	AAI03693	DNA encoding novel
410	15	6.7	767	23	AAI19951	Drosophila melanog	c 483	15	6.7	1636	15	AAQ58006	Human full-length
411	15	6.7	774	22	AAI22106	Human breast cancer	c 484	15	6.7	1660	22	AAI22106	DNA encoding novel
412	15	6.7	780	22	AAI31394	Human CDNA encodin	c 485	15	6.7	1667	22	AAI22106	DNA encoding novel
413	15	6.7	811	21	AAAC49886	Arabidopsis thalia	c 486	15	6.7	1668	23	AAI22106	DNA encoding novel
414	15	6.7	812	21	AAAC49886	Arabidopsis thalia	c 487	15	6.7	1671	22	AAI22106	DNA encoding novel
415	15	6.7	838	22	AAK66649	Human immune/haema	c 488	15	6.7	1691	21	AAI22106	Human secreted pro
416	15	6.7	838	22	AAK71928	Human immune/haema	c 489	15	6.7	1723	22	AAI22106	Aspergillus oryzae
417	15	6.7	850	22	AAH05401	Human CDNA clone (	c 490	15	6.7	1736	22	AAI22106	Human diagnostic a
418	15	6.7	854	21	AAAD00290	Rice histidine bio	c 491	15	6.7	1756	23	ABLI3919	Human CDNA sequenc
419	15	6.7	887	22	AAH31614	Human olfactory re	c 492	15	6.7	1836	24	AAI99435	Drosophila melanog
420	15	6.7	890	22	AAI21953	Human breast cancer	c 493	15	6.7	1862	21	AAI99435	Mouse ischaemic co
421	15	6.7	903	21	AAZ61638	cDNA encoding muri	c 494	15	6.7	1864	21	AAI99435	Arabidopsis thalia
422	15	6.7	903	22	AAZ61638	Skin cell cDNA, SE	c 495	15	6.7	1871	13	AAQ026959	Arabidopsis thalia
423	15	6.7	908	22	AAI24826	Human breast cancer	c 496	15	6.7	1883	23	AAQ026959	Guinea pig PAF rec
424	15	6.7	920	13	AAQ32366	MAGE-10 genomic DN	c 497	15	6.7	1902	22	AAQ026959	DNA encoding novel
425	15	6.7	920	15	AAQ72491	Tumour rejection a	c 498	15	6.7	1914	23	ABL27825	Human full-length
426	15	6.7	920	16	AAQ72491	MAGE-10 gene. Hom	c 499	15	6.7	1932	22	AAI67196	Drosophila melanog
427	15	6.7	920	20	AAH84126	MAGE-10 gene. Hom	c 500	15	6.7	1956	22	AAK29286	Nucleotide sequenc
428	15	6.7	920	21	AAAD01313	Human MAGE-A10 par	c 501	15	6.7	1956	22	AAI13887	Human bone marrow
429	15	6.7	935	22	AAI66460	Human ankyrin 27 c	c 502	15	6.7	1956	22	AAI13887	Probe #3820 for ge
430	15	6.7	957	22	AAH31653	Human olfactory re	c 503	15	6.7	1956	22	AAI13887	Probe #3935 used t
431	15	6.7	960	22	AAH32344	Human olfactory re	c 504	15	6.7	1962	22	AAI03750	Probe #3741 used t
432	15	6.7	976	22	AAK42326	Human bone marrow	c 505	15	6.7	1964	23	AAH84606	Nucleotide sequenc
433	15	6.7	976	22	AAI23105	Human bone marrow	c 506	15	6.7	2029	22	AAH15472	DNA encoding novel
434	15	6.7	976	22	AAI48408	Probe #13038 for g	c 507	15	6.7	2045	22	AAH15472	Human CDNA sequenc
435	15	6.7	976	22	AAI08754	Probe #8745 used t	c 508	15	6.7	2057	22	AAH14091	Human polynucleoti
436	15	6.7	978	22	AAH31933	Human olfactory re	c 509	15	6.7	2086	24	ABA05349	Human CDNA sequenc
437	15	6.7	997	22	AAAD08303	Human secreted pro	c 510	15	6.7	2152	22	AAH33119	Human initiation f
438	15	6.7	1024	21	AAZ97161	Human prostate can	c 511	15	6.7	2156	20	AAI10807	DNA encoding human
439	15	6.7	1024	21	AAZ97161	Human prostate can	c 512	15	6.7	2156	22	AAI10807	Polynucleotide seq
440	15	6.7	1024	22	AAZ97225	Human prostate can	c 513	15	6.7	2156	22	AAI10807	Human CDNA encodin
441	15	6.7	1044	22	AAZ97225	Human CDNA encodin	c 514	15	6.7	2156	24	ABA90932	Human polynucleoti
442	15	6.7	1066	22	AAAD04777	Human death domain	c 515	15	6.7	2168	21	AAI15970	Human protein clon
443	15	6.7	1077	21	AA55224	C. symbiosum open	c 516	15	6.7	2181	23	ABL27979	Drosophila melanog
444	15	6.7	1079	19	AAV41891	Alternatively spli	c 517	15	6.7	2199	21	AAI629538	Human secreted pro
445	15	6.7	1088	19	AAV41890	Nucleotide sequenc	c 518	15	6.7	2209	24	AAI629538	cDNA sequence #609
446	15	6.7	1140	19	AAV71081	Alpha-actinin acti	c 519	15	6.7	2294	22	AAAD08300	Human secreted pro
447	15	6.7	1174	20	AAH87944	Human G protein co	c 520	15	6.7	2372	22	AAI63939	Human CDNA encodin
										2427	15	AAQ70435	Human glyco-protei

521	15	6.7	2474	23	ABL15009	Drosophila melanog	594	15	6.7	4499	22	AAI58788	Human polynucleoti
522	15	6.7	2488	22	AAH17612	Human cDNA sequenc	595	15	6.7	4499	22	AAI58789	Human polynucleoti
523	15	6.7	2541	23	ABL11368	Drosophila melanog	596	15	6.7	4586	22	AAI60573	Human polynucleoti
524	15	6.7	2548	23	ABL27826	Drosophila melanog	597	15	6.7	4586	22	AAI60574	Human polynucleoti
525	15	6.7	2559	19	AAV26618	MAGE-10 tumour rej	598	15	6.7	4586	22	AAI60575	Human polynucleoti
526	15	6.7	2559	21	AAAD01312	Human MAGE-A10 cDN	599	15	6.7	4616	22	AAH98704	Human EST-derived
527	15	6.7	2559	21	AAAS2965	Human tumour rejec	600	15	6.7	4636	19	AAV23920	Human alpha3 integ
528	15	6.7	2560	21	AAAT75111	cDNA encoding a hu	601	15	6.7	4636	19	AAV23920	Human alpha3 integ
529	15	6.7	2603	22	AAH13930	Human cDNA sequenc	602	15	6.7	4881	23	ABL15008	Drosophila melanog
530	15	6.7	2610	24	AAAS96324	Arabidopsis cDNA e	603	15	6.7	4702	23	ABL09844	Drosophila melanog
531	15	6.7	2673	9	AAH21199	ENVRN sequence fro	604	15	6.7	4724	23	AAI58787	Human polynucleoti
532	15	6.7	2688	23	ABL07343	Drosophila melanog	605	15	6.7	4825	23	ABL07342	Drosophila melanog
533	15	6.7	2742	23	AAAS1581	Pseudomonas aerugi	606	15	6.7	4867	23	ABL07564	Drosophila melanog
534	15	6.7	2757	22	AAAS26875	Human cDNA encodin	607	15	6.7	4886	21	AAH76173	Human ORF ORF1728
535	15	6.7	2757	23	ABL23365	Drosophila melanog	608	15	6.7	4907	22	AAAF26592	DNA encoding huma
536	15	6.7	2812	22	AAH78486	Human immune/haema	609	15	6.7	5176	19	AAV04017	Human multiple mye
537	15	6.7	2856	23	ABL22267	Drosophila melanog	610	15	6.7	5456	22	AAAS2580	Human polynucleoti
538	15	6.7	2895	22	AAAF32642	Human cDNA encodin	611	15	6.7	5499	22	AAH67617	Human immune/haema
539	15	6.7	2903	23	AAH78152	DNA encoding novel	612	15	6.7	5672	23	ABL13120	Drosophila melanog
540	15	6.7	2919	21	AAZ90526	Human GPCR protein	613	15	6.7	5714	22	AAAS08649	Human cDNA encodin
541	15	6.7	2929	21	AAZ52366	NS5Q gene-18 assoc	614	15	6.7	5714	22	AAAS08659	Human cDNA encodin
542	15	6.7	2973	22	AAH17771	Human cDNA sequenc	615	15	6.7	5726	22	AAH98377	Human EST-derived
543	15	6.7	2997	22	AAK94769	Human full-length	616	15	6.7	5773	22	AAAS08648	Human cDNA encodin
544	15	6.7	3000	21	AAZ87930	Human brain-derive	617	15	6.7	5805	23	ABL22266	Drosophila melanog
545	15	6.7	3001	23	AAH88249	CNS disorder-relat	618	15	6.7	6096	22	AAAS26766	Human genomic DNA
546	15	6.7	3015	23	ABL04274	Drosophila melanog	619	15	6.7	6197	22	AAK85057	Human immune/haema
547	15	6.7	3072	21	AAAF16331	Human prostate can	620	15	6.7	6198	22	AAK85054	Human immune/haema
548	15	6.7	3081	22	ABAB26677	Alpha-actinin (ACT	621	15	6.7	6200	22	AAK85058	Human immune/haema
549	15	6.7	3092	21	AAAF18291	Lung cancer associ	622	15	6.7	6201	22	AAK85056	Human immune/haema
550	15	6.7	3095	22	AAK82207	Human immune/haema	623	15	6.7	6234	20	AAZ20522	Polynucleotide seq
551	15	6.7	3127	23	AAH03828	Drosophila melanog	624	15	6.7	6240	23	ABL07542	Drosophila melanog
552	15	6.7	3143	22	AAI61342	Human polynucleoti	625	15	6.7	6313	23	ABL23364	Drosophila melanog
553	15	6.7	3144	23	ABL19950	Drosophila melanog	626	15	6.7	6449	23	ABL14133	Drosophila melanog
554	15	6.7	3334	22	AAK82796	Human immune/haema	627	15	6.7	6454	22	AAI57932	Human polynucleoti
555	15	6.7	3399	21	AAAG99113	Human pancreatic c	628	15	6.7	6502	22	AAH98718	Human late stage o
556	15	6.7	3447	23	ABL16117	Drosophila melanog	629	15	6.7	6529	19	AAV41889	Nucleotide sequenc
557	15	6.7	3472	23	AAH72696	DNA encoding novel	630	15	6.7	6610	23	ABL16116	Drosophila melanog
558	15	6.7	3504	22	AAH15784	Human cDNA sequenc	631	15	6.7	6645	17	AAAT65002	Mouse cell cycle r
559	15	6.7	3510	21	AAAD01311	Human MAGE-A10 gen	632	15	6.7	6742	22	AAI59718	Human polynucleoti
560	15	6.7	3543	23	ABL07543	Drosophila melanog	633	15	6.7	7156	22	AAK86021	Human immune/haema
561	15	6.7	3561	23	AAAS76613	DNA encoding novel	634	15	6.7	7156	22	AAK86022	Human immune/haema
562	15	6.7	3566	23	ABL07518	Drosophila melanog	635	15	6.7	7319	24	AAAS4894	Human DNA sequence
563	15	6.7	3689	22	ABAB3088	DFZps860031 ovar	636	15	6.7	7640	22	AAK91239	Human digestive sy
564	15	6.7	3707	22	AAAF80532	Receptor #20 parti	637	15	6.7	7961	23	ABL27070	Drosophila melanog
565	15	6.7	3736	22	AAK85055	Human immune/haema	638	15	6.7	7964	23	ABL19500	Drosophila melanog
566	15	6.7	3762	22	AAK76204	Human immune/haema	639	15	6.7	7971	12	AAK74473	Human immune/haema
567	15	6.7	3825	22	AAAS01561	Human secretory mo	640	15	6.7	8174	18	AAQ56908	DNA encoding a gly
568	15	6.7	3914	23	ABL27824	Drosophila melanog	641	15	6.7	8174	18	AAQ56908	DNA encoding a gly
569	15	6.7	3923	23	ABL21916	Drosophila melanog	642	15	6.7	8396	21	AAZ59353	Human alpha(1,2)-f
570	15	6.7	3950	20	AAZ34259	Human PRO768 nucle	643	15	6.7	8764	22	AAK91240	Human STP2 (phenol
571	15	6.7	3951	21	AAZ78566	Human PRO768 (UNQ4	644	15	6.7	9149	23	ABL14132	Human digestive sy
572	15	6.7	3951	22	AAAS45984	Human DNA encoding	645	15	6.7	9473	10	AAH92768	Drosophila melanog
573	15	6.7	3977	24	ABL01591	Human secreted pro	646	15	6.7	9630	21	AAZ89628	HIV-2 variant HIV-
574	15	6.7	3989	20	AAV84428	Human secreted pro	647	15	6.7	9630	21	AAZ89628	HIV-2 variant HIV-
575	15	6.7	3989	22	ABAB3211	Human secreted pro	648	15	6.7	9643	9	AAH80859	Sequence of entire
576	15	6.7	4024	23	ABL05958	Drosophila melanog	649	15	6.7	9663	21	AAH81938	Packaging vector p
577	15	6.7	4032	22	AAAF90327	Human JAFFA genom	650	15	6.7	9672	13	AAQ20616	ROD HIV-2 isolate
578	15	6.7	4042	22	AAK51596	Human polynucleoti	651	15	6.7	9726	21	AAH81937	Packaging vector p
579	15	6.7	4080	22	AAAC83438	Human integrin alp	652	15	6.7	9931	23	ABL17306	Drosophila melanog
580	15	6.7	4102	22	AAAS01489	Human secreted pro	653	15	6.7	10163	18	AAH61085	Full-length HIV-2K
581	15	6.7	4181	23	ABL21702	Drosophila melanog	654	15	6.7	10290	23	ABL27978	Drosophila melanog
582	15	6.7	4204	21	AAH81925	Vector pCM-ENV(ROD	655	15	6.7	10577	22	AAK72646	Human immune/haema
583	15	6.7	4204	21	AAH81939	Envelope vector pC	656	15	6.7	11136	23	ABL16298	Drosophila melanog
584	15	6.7	4276	23	ABL17383	Drosophila melanog	657	15	6.7	11869	22	AAAS36792	Human cardiovascular
585	15	6.7	4300	23	ABL17307	Drosophila melanog	658	15	6.7	11987	22	AAI07284	Human reproductive
586	15	6.7	4310	19	AAV34856	Drosophila melanog	659	15	6.7	12112	22	AAK83784	Human immune/haema
587	15	6.7	4340	23	ABL13918	Drosophila melanog	660	15	6.7	12259	22	AAAS36190	Human cardiovascular
588	15	6.7	4350	22	AAAD09490	Human immunodefici	661	15	6.7	12807	22	AAH05769	Human reproductive
589	15	6.7	4375	22	AAAS63188	Human purified sec	662	15	6.7	14333	22	AAK79846	Human immune/haema
590	15	6.7	4382	22	AAAS44669	Human full-length	663	15	6.7	14825	23	ABL17382	Drosophila melanog
591	15	6.7	4406	23	ABL03692	Drosophila melanog	664	15	6.7	14918	22	AAAS26792	Human genomic DNA
592	15	6.7	4443	22	AAH57448	Human lung cell sp	665	15	6.7	16983	23	AAK85126	Human immune/haema
593	15	6.7	4487	23	ABL15982	Drosophila melanog	666	15	6.7	17464	23	ABL03994	Drosophila melanog
										18974	21	AAH81485	N. meningitidis pa

c 667	15	6.7	20072	20	AA13026	Enterococcus faeca	c 740	14	6.2	241	19	AAV46145	Human HLA-A intron
c 668	15	6.7	21313	22	AAK82710	Human immune/haema	c 741	14	6.2	241	19	AAV46146	Human HLA-A intron
c 669	15	6.7	22465	22	AAK86932	Human immune/haema	c 742	14	6.2	241	19	AAV46147	Human HLA-A intron
c 670	15	6.7	22585	22	AA104299	Human reproductive	c 743	14	6.2	241	19	AAV46148	Human HLA-A intron
c 671	15	6.7	26225	22	AA35776	Human cardiovascular	c 744	14	6.2	241	19	AAV46149	Human HLA-A intron
c 672	15	6.7	32958	21	AA55186	Cenarchaeum symbio	c 745	14	6.2	241	19	AAV46150	Human HLA-A intron
c 673	15	6.7	33780	22	AAH24652	Nucleotide sequenc	c 746	14	6.2	241	19	AAV46151	Human HLA-A intron
c 674	15	6.7	35829	23	AA559573	Propionibacterium	c 747	14	6.2	241	19	AAV46152	Human HLA-A intron
c 675	15	6.7	36519	19	AAV22141	Chimpanzee adenovi	c 748	14	6.2	241	19	AAV46153	Human HLA-A intron
c 676	15	6.7	38059	22	AAF54018	Human factor IX (h	c 749	14	6.2	241	19	AAV46134	Human HLA-A intron
c 677	15	6.7	42979	23	ABL20870	Drosophila melanog	c 750	14	6.2	241	19	AAV46135	Human HLA-A intron
c 678	15	6.7	45265	21	AAZ46508	Sequence of a COSM	c 751	14	6.2	241	19	AAV46136	Human HLA-A intron
c 679	15	6.7	49999	20	AAZ23303	Human LOBO homolog	c 752	14	6.2	241	19	AAV46137	Human HLA-A intron
c 680	15	6.7	50000	20	AAZ23517	Human kidney amino	c 753	14	6.2	241	19	AAV46138	Human HLA-A intron
c 681	15	6.7	56583	21	AAF21125	Human low adenosin	c 754	14	6.2	241	19	AAV46139	Human HLA-A intron
c 682	15	6.7	56583	21	AAA35003	Human adenosine re	c 755	14	6.2	241	19	AAV46140	Human HLA-A intron
c 683	15	6.7	61313	23	AA559545	Propionibacterium	c 756	14	6.2	241	19	AAV46141	Human HLA-A intron
c 684	15	6.7	72049	22	ABA82623	Human HBM gene reg	c 757	14	6.2	241	19	AAV46121	Human HLA-A intron
c 685	15	6.7	74962	22	AD15256	Human phosphatase	c 758	14	6.2	241	19	AAV46122	Human HLA-A intron
c 686	15	6.7	125910	21	AAC64370	Human KCMQ5 (KCM6q	c 759	14	6.2	241	19	AAV46123	Human HLA-A intron
c 687	15	6.7	305107	22	AAH62689	Shrimp white spot	c 760	14	6.2	241	19	AAV46117	Human HLA-A intron
c 688	15	6.7	349980	21	AAF21607	Neisseria meningit	c 761	14	6.2	241	19	AAV46119	Human HLA-A intron
c 689	15	6.7	349980	22	AAH68531	C glutamicum codin	c 762	14	6.2	241	19	AAV46120	Human HLA-A intron
c 690	15	6.7	1230025	20	AA91990	Nucleotide sequenc	c 763	14	6.2	241	19	AAV46121	Human HLA-A intron
c 691	15	6.7	1437668	21	AA81490	N. meningitidis B	c 764	14	6.2	241	19	AAV46122	Human HLA-A intron
c 692	14	6.2	18	22	AAF81317	Human cacng8 PCR p	c 765	14	6.2	241	19	AAV46123	Human HLA-A intron
c 693	14	6.2	20	21	AAC80118	Reverse primer #30	c 766	14	6.2	241	19	AAV46124	Human HLA-A intron
c 694	14	6.2	20	22	AAD06140	Human MAGF-A12 gen	c 767	14	6.2	241	19	AAV46125	Human HLA-A intron
c 695	14	6.2	20	24	ABI97419	Capture oligonucle	c 768	14	6.2	241	19	AAV46126	Human HLA-A intron
c 696	14	6.2	21	21	AAC80113	Reverse primer #25	c 769	14	6.2	241	19	AAV46127	Human HLA-A intron
c 697	14	6.2	21	21	AAC80119	Reverse primer #31	c 770	14	6.2	241	19	AAV46128	Human HLA-A intron
c 698	14	6.2	21	21	AAC36933	Reverse primer #27	c 771	14	6.2	241	19	AAV46129	Human HLA-A intron
c 699	14	6.2	21	21	AAAL1478	Reverse primer #33	c 772	14	6.2	241	19	AAV46130	Human HLA-A intron
c 700	14	6.2	22	21	AAC80114	Reverse primer #26	c 773	14	6.2	241	19	AAV46106	Human HLA-A intron
c 701	14	6.2	22	21	AAC80120	Reverse primer #32	c 774	14	6.2	241	19	AAV46107	Human HLA-A intron
c 702	14	6.2	23	21	AAC80115	Reverse primer #27	c 775	14	6.2	241	19	AAV46108	Human HLA-A intron
c 703	14	6.2	23	21	AAC80121	Reverse primer #33	c 776	14	6.2	241	19	AAV46109	Human HLA-A intron
c 704	14	6.2	24	21	AAC80116	Reverse primer #28	c 777	14	6.2	241	19	AAV46111	Human HLA-A intron
c 705	14	6.2	24	21	AAC80122	Reverse primer #34	c 778	14	6.2	241	19	AAV46112	Human HLA-A intron
c 706	14	6.2	24	24	ABI91408	Capture oligonucle	c 779	14	6.2	241	19	AAV46113	Human HLA-A intron
c 707	14	6.2	24	24	ABI91409	Capture oligonucle	c 780	14	6.2	241	19	AAV46114	Human HLA-A intron
c 708	14	6.2	25	21	AAC80117	Reverse primer #29	c 781	14	6.2	241	19	AAV46115	Human HLA-A intron
c 709	14	6.2	25	21	AAC80123	Reverse primer #35	c 782	14	6.2	241	19	AAV46116	Human HLA-A intron
c 710	14	6.2	38	21	AAAL1526	Drosophila sp. TGF	c 783	14	6.2	241	20	AAV46116	Human HLA-A intron
c 711	14	6.2	49	24	AAI67605	MAGE-1 DNA fragmen	c 784	14	6.2	241	20	AAV46116	Human HLA-A intron
c 712	14	6.2	50	13	AAQ28134	Human T lymphocyte	c 785	14	6.2	241	20	AAV46116	Human HLA-A intron
c 713	14	6.2	81	16	AAV04790	TCR CDR3 V-alpha r	c 786	14	6.2	241	20	AAV46116	Human HLA-A intron
c 714	14	6.2	122	18	AAV02805	Human RHAMM genom	c 787	14	6.2	241	20	AAV46116	Human HLA-A intron
c 715	14	6.2	130	22	ABAL1561	Human nervous syst	c 788	14	6.2	241	20	AAV46116	Human HLA-A intron
c 716	14	6.2	144	22	ABAL15314	Human brain expres	c 789	14	6.2	241	20	AAV46116	Human HLA-A intron
c 717	14	6.2	144	22	AAK41035	Human bone marrow	c 790	14	6.2	241	20	AAV46116	Human HLA-A intron
c 718	14	6.2	158	16	AAAT20252	Human gene signatu	c 791	14	6.2	241	20	AAV46116	Human HLA-A intron
c 719	14	6.2	158	21	AAAC15608	Human secreted pro	c 792	14	6.2	241	20	AAV46116	Human HLA-A intron
c 720	14	6.2	165	16	AAQ98921	TGF-beta inducible	c 793	14	6.2	241	20	AAV46116	Human HLA-A intron
c 721	14	6.2	177	19	AAQ10468	Human biallelic po	c 794	14	6.2	241	20	AAV46116	Human HLA-A intron
c 722	14	6.2	177	20	AAAL18098	Coding sequence fo	c 795	14	6.2	241	20	AAV46116	Human HLA-A intron
c 723	14	6.2	181	22	AAAC3961	Human prostate cDN	c 796	14	6.2	241	20	AAV46116	Human HLA-A intron
c 724	14	6.2	181	22	AAAC3962	Human prostate cDN	c 797	14	6.2	241	20	AAV46116	Human HLA-A intron
c 725	14	6.2	211	21	AAAC10642	Human secreted pro	c 798	14	6.2	241	20	AAV46116	Human HLA-A intron
c 726	14	6.2	219	19	AAAL1713	Human biallelic po	c 799	14	6.2	241	20	AAV46116	Human HLA-A intron
c 727	14	6.2	219	19	AAAL1713	Human biallelic po	c 800	14	6.2	241	20	AAV46116	Human HLA-A intron
c 728	14	6.2	223	16	AAAT01041	Mouse B7-2 exon m	c 801	14	6.2	241	20	AAV46116	Human HLA-A intron
c 729	14	6.2	231	21	AAZ80203	Human colon cancer	c 802	14	6.2	241	20	AAV46116	Human HLA-A intron
c 730	14	6.2	235	20	AAV37976	Histocompatibility	c 803	14	6.2	241	20	AAV46116	Human HLA-A intron
c 731	14	6.2	240	19	AAV46152	Human HLA-A intron	c 804	14	6.2	241	20	AAV46116	Human HLA-A intron
c 732	14	6.2	240	21	AAC80402	HLA-A intron 2 seq	c 805	14	6.2	241	20	AAV46116	Human HLA-A intron
c 733	14	6.2	240	21	AAC80407	HLA-A intron 2 seq	c 806	14	6.2	241	20	AAV46116	Human HLA-A intron
c 734	14	6.2	240	21	AAC80408	HLA-A intron 2 seq	c 807	14	6.2	241	20	AAV46116	Human HLA-A intron
c 735	14	6.2	240	21	AAC80409	HLA-A intron 2 seq	c 808	14	6.2	241	20	AAV46116	Human HLA-A intron
c 736	14	6.2	240	21	AAC80410	HLA-A intron 2 seq	c 809	14	6.2	241	20	AAV46116	Human HLA-A intron
c 737	14	6.2	241	19	AAV46142	Human HLA-A intron	c 810	14	6.2	241	20	AAV46116	Human HLA-A intron
c 738	14	6.2	241	19	AAV46143	Human HLA-A intron	c 811	14	6.2	241	20	AAV46116	Human HLA-A intron
c 739	14	6.2	241	19	AAV46144	Human HLA-A intron	c 812	14	6.2	241	20	AAV46116	Human HLA-A intron



C 813	14	6.2	241	20	AA37941	Histocompatibility	C 886	14	6.2	325	22	AAI21438	Probe #11371 for g
C 814	14	6.2	241	20	AA37942	Histocompatibility	C 887	14	6.2	325	22	AAI46727	Probe #15413 used t
C 815	14	6.2	241	20	AA37943	Histocompatibility	C 888	14	6.2	325	22	AAI07133	Human secreted pro
C 816	14	6.2	241	20	AA37944	Histocompatibility	889	14	6.2	330	21	AA233145	Human polynucleoti
C 817	14	6.2	241	20	AA37945	Histocompatibility	890	14	6.2	332	22	AAI88816	Human immune/haema
C 818	14	6.2	241	20	AA37946	Histocompatibility	891	14	6.2	334	22	AAK56289	M. tuberculosis an
C 819	14	6.2	241	20	AA37947	Histocompatibility	C 892	14	6.2	339	20	AAZ19382	M. tuberculosis re
C 820	14	6.2	241	20	AA37948	Histocompatibility	C 893	14	6.2	339	20	AAZ19170	M. tuberculosis an
C 821	14	6.2	241	20	AA37949	Histocompatibility	C 894	14	6.2	339	22	AA03814	Human immune/haema
C 822	14	6.2	241	20	AA37950	Histocompatibility	C 895	14	6.2	347	22	AAK72458	Human immune/haema
C 823	14	6.2	241	20	AA37951	Histocompatibility	C 896	14	6.2	347	22	AAK72459	Human immune/haema
C 824	14	6.2	241	20	AA37952	Histocompatibility	C 897	14	6.2	347	22	AAK72460	Human immune/haema
C 825	14	6.2	241	20	AA37953	Histocompatibility	C 898	14	6.2	350	22	AAK58335	Human cardiovascular
C 826	14	6.2	241	20	AA37954	Histocompatibility	C 899	14	6.2	350	22	AAK58317	Human immune/haema
C 827	14	6.2	241	20	AA37955	Histocompatibility	900	14	6.2	358	19	AAV66399	cDNA clone H47990.
C 828	14	6.2	241	20	AA37956	Histocompatibility	C 901	14	6.2	359	21	AA03546	Human secreted pro
C 829	14	6.2	241	21	AA03936	HLA-A intron 2 seq	902	14	6.2	361	22	ABA48981	Human breast cell
C 830	14	6.2	241	21	AA03937	HLA-A intron 2 seq	903	14	6.2	361	22	ABA33974	Probe #12440 for g
C 831	14	6.2	241	21	AA03938	HLA-A intron 2 seq	904	14	6.2	361	22	AAI21826	Probe #11759 for g
C 832	14	6.2	241	21	AA03939	HLA-A intron 2 seq	905	14	6.2	361	22	AAI47112	Probe #15798 used
C 833	14	6.2	241	21	AA03940	HLA-A intron 2 seq	906	14	6.2	361	22	AAI07513	Probe #7504 used t
C 834	14	6.2	241	21	AA03941	HLA-A intron 2 seq	907	14	6.2	369	14	AAQ59994	Human brain expres
C 835	14	6.2	241	21	AA03942	HLA-A intron 2 seq	908	14	6.2	369	22	ABA50866	Human breast cell
C 836	14	6.2	241	21	AA03943	HLA-A intron 2 seq	C 909	14	6.2	369	22	ABA68840	Human foetal liver
C 837	14	6.2	241	21	AA03944	HLA-A intron 2 seq	C 910	14	6.2	369	22	ABA35790	Probe #14256 for g
C 838	14	6.2	241	21	AA03945	HLA-A intron 2 seq	C 911	14	6.2	369	22	AAK11775	Human brain expres
C 839	14	6.2	241	21	AA03946	HLA-A intron 2 seq	C 912	14	6.2	369	22	AAK42958	Human bone marrow
C 840	14	6.2	241	21	AA03947	HLA-A intron 2 seq	C 913	14	6.2	369	22	AAI23723	Probe #13656 for g
C 841	14	6.2	241	21	AA03948	HLA-A intron 2 seq	C 914	14	6.2	369	22	AAI49036	Probe #17722 used
C 842	14	6.2	241	21	AA03949	HLA-A intron 2 seq	C 915	14	6.2	369	22	AAI09339	Probe #9330 used t
C 843	14	6.2	241	21	AA03950	HLA-A intron 2 seq	C 916	14	6.2	371	22	AAK88949	Human digestive sy
C 844	14	6.2	241	21	AA03951	HLA-A intron 2 seq	917	14	6.2	372	16	AAI26549	Human gene signatu
C 845	14	6.2	241	21	AA03952	HLA-A intron 2 seq	918	14	6.2	377	19	AAV17747	Human breast cance
C 846	14	6.2	241	21	AA03953	HLA-A intron 2 seq	C 919	14	6.2	377	22	AAI81618	Human polynucleoti
C 847	14	6.2	241	21	AA03954	HLA-A intron 2 seq	C 920	14	6.2	378	22	AAK63042	Human immune/haema
C 848	14	6.2	241	21	AA03955	HLA-A intron 2 seq	921	14	6.2	382	22	AAI84492	Human polynucleoti
C 849	14	6.2	241	21	AA03956	HLA-A intron 2 seq	922	14	6.2	384	22	AAI17650	Human breast cance
C 850	14	6.2	241	21	AA03957	HLA-A intron 2 seq	923	14	6.2	384	22	AAI18686	Human breast cance
C 851	14	6.2	241	21	AA03958	HLA-A intron 2 seq	924	14	6.2	385	22	AAI10922	Human breast cance
C 852	14	6.2	241	21	AA03959	HLA-A intron 2 seq	925	14	6.2	389	21	AAK80652	Human secreted pro
C 853	14	6.2	241	21	AA03960	HLA-A intron 2 seq	926	14	6.2	390	22	AAK65045	Human secreted pro
C 854	14	6.2	241	21	AA03961	HLA-A intron 2 seq	927	14	6.2	393	22	AAK66699	Novel human polynu
C 855	14	6.2	241	21	AA03962	HLA-A intron 2 seq	928	14	6.2	394	14	AAQ60760	Novel human polynu
C 856	14	6.2	241	21	AA03963	HLA-A intron 2 seq	929	14	6.2	395	22	AAI86496	Human brain expres
C 857	14	6.2	241	21	AA03964	HLA-A intron 2 seq	930	14	6.2	398	22	AAI83317	Human polynucleoti
C 858	14	6.2	241	21	AA03965	HLA-A intron 2 seq	C 931	14	6.2	399	20	AAK41514	Human secreted pro
C 859	14	6.2	241	21	AA03966	HLA-A intron 2 seq	932	14	6.2	401	22	AAK95984	Human secreted pro
C 860	14	6.2	241	21	AA03967	HLA-A intron 2 seq	933	14	6.2	401	22	AAK97477	Human neurogulin g
C 861	14	6.2	241	21	AA03968	HLA-A intron 2 seq	C 934	14	6.2	401	22	AAK40316	DNA encoding human
C 862	14	6.2	241	21	AA03969	HLA-A intron 2 seq	C 935	14	6.2	401	22	AAK03916	Human reproductive
C 863	14	6.2	241	21	AA03970	HLA-A intron 2 seq	936	14	6.2	404	21	AAK08931	Human secreted pro
C 864	14	6.2	241	21	AA03971	HLA-A intron 2 seq	C 937	14	6.2	405	21	AAK25365	Human secreted pro
C 865	14	6.2	241	21	AA03972	HLA-A intron 2 seq	938	14	6.2	406	22	AAK20753	Human breast cance
C 866	14	6.2	241	21	AA03973	HLA-A intron 2 seq	939	14	6.2	406	23	AAK84227	DNA encoding novel
C 867	14	6.2	241	21	AA03974	HLA-A intron 2 seq	940	14	6.2	407	22	AAK66214	Novel human polynu
C 868	14	6.2	241	21	AA03975	HLA-A intron 2 seq	941	14	6.2	408	22	AAK11863	Human breast cance
C 869	14	6.2	241	21	AA03976	HLA-A intron 2 seq	C 942	14	6.2	408	22	AAI191810	Human polynucleoti
C 870	14	6.2	241	21	AA03977	HLA-A intron 2 seq	C 943	14	6.2	413	22	AAI23872	Human breast cance
C 871	14	6.2	241	21	AA03978	HLA-A intron 2 seq	944	14	6.2	413	22	AAI192167	Human polynucleoti
C 872	14	6.2	241	21	AA03979	HLA-A intron 2 seq	C 945	14	6.2	414	22	AAI15019	Human breast cance
C 873	14	6.2	241	21	AA03980	HLA-A intron 2 seq	C 946	14	6.2	416	21	AAK29486	Incute clone 12110
C 874	14	6.2	241	21	AA03981	HLA-A intron 2 seq	C 947	14	6.2	416	22	ABA72539	Human foetal liver
C 875	14	6.2	241	21	AA03982	HLA-A intron 2 seq	C 948	14	6.2	416	22	ABA38282	Probe #16748 for g
C 876	14	6.2	241	21	AA03983	HLA-A intron 2 seq	C 949	14	6.2	416	22	AAK20963	Human brain expres
C 877	14	6.2	241	21	AA03984	HLA-A intron 2 seq	C 950	14	6.2	416	22	AAK47116	Human bone marrow
C 878	14	6.2	241	21	AA03985	HLA-A intron 2 seq	C 951	14	6.2	416	22	AAI52952	Probe #21638 used
C 879	14	6.2	241	21	AA03986	HLA-A intron 2 seq	C 952	14	6.2	416	23	AAK87970	DNA encoding novel
C 880	14	6.2	241	21	AA03987	HLA-A intron 2 seq	953	14	6.2	417	21	AAK22774	Human secreted pro
C 881	14	6.2	241	21	AA03988	HLA-A intron 2 seq	954	14	6.2	422	22	ABA45497	Human breast cell
C 882	14	6.2	241	21	AA03989	HLA-A intron 2 seq	955	14	6.2	422	23	AAK66872	DNA encoding nove
C 883	14	6.2	241	21	AA03990	HLA-A intron 2 seq	C 956	14	6.2	425	22	AAK39470	cDNA encoding nove
C 884	14	6.2	241	21	AA03991	HLA-A intron 2 seq	C 957	14	6.2	425	22	AAK88337	Human digestive sy
C 885	14	6.2	241	21	AA03992	HLA-A intron 2 seq	C 958	14	6.2	427	22	AAK73686	Human immune/haema

c 959 14 6.2 427 22 AAK73697 Human immune/haema  
 c 960 14 6.2 430 22 AAL26228 Human breast cancer  
 c 961 14 6.2 431 22 AAI181528 Human polynucleoti  
 c 962 14 6.2 431 22 AAL23701 Human TSG16 altern  
 c 963 14 6.2 433 21 AAC18224 Human secreted pro  
 c 964 14 6.2 435 22 AAL10575 Human breast cance  
 c 965 14 6.2 438 22 AAL24370 Human breast cance  
 c 966 14 6.2 439 22 AAH35537 Human colon cancer  
 c 967 14 6.2 441 21 AAC17357 Human secreted pro  
 c 968 14 6.2 442 22 AAL05342 Human reproductive  
 c 969 14 6.2 442 22 AAI188119 Human polynucleoti  
 c 970 14 6.2 443 22 AAL05343 Human reproductive  
 c 971 14 6.2 443 22 AAI56170 Probe #24856 used  
 c 972 14 6.2 444 22 AAK60629 Human immune/haema  
 c 973 14 6.2 449 22 AAL01530 Human reproductive  
 c 974 14 6.2 450 22 ABA43707 Human breast cell  
 c 975 14 6.2 450 22 ABA54164 Human foetal liver  
 c 976 14 6.2 450 22 ABA23909 Probe #2375 for ge  
 c 977 14 6.2 450 22 AAK02434 Human brain expres  
 c 978 14 6.2 450 22 AAK27875 Human bone marrow  
 c 979 14 6.2 450 22 AAI12456 Probe #2389 for ge  
 c 980 14 6.2 450 22 AAI33810 Probe #2496 used t  
 c 981 14 6.2 450 22 AAI02367 Probe #2358 used t  
 c 982 14 6.2 455 22 ABA43495 Human breast cell  
 c 983 14 6.2 455 22 ABA53943 Human foetal liver  
 c 984 14 6.2 455 22 ABA23694 Probe #2160 for ge  
 c 985 14 6.2 455 22 AAK02213 Human brain expres  
 c 986 14 6.2 455 22 AAK27660 Human bone marrow  
 c 987 14 6.2 455 22 AAK30316 Human bone marrow  
 c 988 14 6.2 455 22 AAI12241 Probe #2174 for ge  
 c 989 14 6.2 455 22 AAI14920 Probe #4853 for ge  
 c 990 14 6.2 455 22 AAI33595 Probe #2281 used t  
 c 991 14 6.2 455 22 AAI02154 Probe #2145 used t  
 c 992 14 6.2 455 22 AAI04697 Probe #4688 used t  
 c 993 14 6.2 456 24 ABA02988 Human ubiquitin co  
 c 994 14 6.2 458 21 ABA31094 Plant microsatelli  
 c 995 14 6.2 458 22 AAS47119 Human breast cance  
 c 996 14 6.2 458 22 AAI17689 Human breast cance  
 c 997 14 6.2 459 22 ABA57002 Human foetal liver  
 c 998 14 6.2 459 22 AAK05066 Human brain expres  
 c 999 14 6.2 459 22 AAK30616 Human bone marrow  
 c1000 14 6.2 461 22 ABA55533 Human foetal liver

## ALIGNMENTS

RESULT 1  
 ID AAK32362 standard; DNA; 225 BP.  
 XX AC AAK32362;  
 XX DT 22-APR-1993 (first entry)  
 XX DE MAGE-6 gene.  
 XX KW Melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;  
 KW tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.  
 XX OS Homo sapiens.  
 XX PN WO9220356-A.  
 XX PD 26-NOV-1992.  
 XX PF 22-MAY-1992; 92WO-US04354.  
 XX PR 23-MAY-1991; 91US-0705702.  
 PR 09-JUL-1991; 91US-0728838.  
 PR 23-SEP-1991; 91US-0764364.  
 PR 12-DEC-1991; 91US-0807043.

PA (LUDW-) LUDWIG INST CANCER RES.  
 XX Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;  
 PI Van Den Eynde B, Van Der Bruggen P, Van Pel A;  
 DR WPI; 1992-415460/50.  
 XX Nucleic acid mol. encoding a human tumour rejection antigen  
 PT precursor - useful as an immunostimulant in a vaccine for  
 PT treating and preventing cancers, also useful in diagnosis  
 XX Disclosure; Page 88; 142pp; English.  
 PS The sequences given in AAK32352-69 represent a new family of genes  
 CC referred to as melanoma antigens (MAGE). The cDNAs of this gene  
 CC family were identified during the isolation of the antigen E gene.  
 CC The MAGE cDNAs, when tested, did not transfer expression of antigen  
 CC E, but they did show substantial homology to the antigen E cDNA  
 CC sequence. The MAGE DNAs share a certain degree of homology with each  
 CC other and are expressed in tumour cells including several types of  
 CC human tumor cells as well as in human tumors. MAGE expression is not  
 CC restricted to melanomas. MAGE refers to a family of tumor rejection  
 CC antigen precursors. The antigens resulting from these genes are  
 CC referred to as MAGE TRAs or melanoma antigen tumor rejection antigens.  
 CC See also AAK32351.  
 XX SQ Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;  
 Query Match 100.0%; Score 225; DB 13; Length 225;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-105;  
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TATTCTTCTCCTGTGATCTTCACCAAGCTTCCGATTCCTTGAGCTGGTCTTTGGCATC 60  
 Db 1 tatttttctctgtgatcttccaaagcttcgattcctcttgagcttggtctttggcatc 60  
 QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTC 120  
 Db 61 gagctgatggaagtggaccccatcgccacgtgtacatctttgccacctgacctgggacctc 120  
 QY 121 TCCTACATGGCGCTGCTGGGTGACATCAGATCATGCCAGGACAGCGTTCTCTGATAATC 180  
 Db 121 tctacatggcctgctgggtgacatcagatcatgccaggacagagcttctctgataatc 180  
 QY 181 ATCTCGGCATATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225  
 Db 181 atctcggccataatcgaagagaggcgactgtgccccctgaggag 225

RESULT 2  
 AAK72487  
 ID AAK72487 standard; cDNA to mRNA; 225 BP.  
 XX AC AAK72487;  
 XX DT 22-JUN-1995 (first entry)  
 XX DE Tumour rejection antigen MAGE-6 cDNA.  
 XX KW Tumour rejection antigen; melanoma antigen-6; MAGE-6; MAGE-3;  
 KW cancer; cytolytic T cells; antigen D; human leucocyte antigen;  
 KW ss.  
 XX OS Homo sapiens.  
 XX PN WO9423031-A.  
 XX PD 13-OCT-1994.  
 XX PF 17-MAR-1994; 94WO-US02877.  
 XX PR 26-MAR-1993; 93US-0037230.

```

XX (LUDW-) LUDWIG INST CANCER RES.
XX PA
XX Boon-falleur T, Gaugler B, Van Den EYNDE B, Van Der BRUGGEN P;
XX PI
XX WPI; 1994-333192/41.
XX DR
XX New tumour rejection antigen precursor MAGE3 - useful in
XX PT treatment and diagnosis of cancer
XX PS
XX Example 32; Page 73; 105pp; English.
XX PS
XX AA072487 is the cDNA sequence which codes for melanoma antigen-6
XX CC (MAGE-6). Another melanoma antigen MAGE-3 is encoded by
XX CC AAQ72470, this is a tumour rejection antigen precursor. Melanomas
XX CC characterised by the expression of MAGE-3 can be detected, or
XX CC monitored, by contacting a test sample with an agent that can
XX CC recognise MAGE-3. The melanoma can be treated by the administration
XX CC of cytolytic T cells specific for the complex of antigen D (the
XX CC mature rejection antigen derived from MAGE-3) and a human leucocyte
XX CC antigen (esp. HLA-A1).
XX SQ
XX Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 15; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.le-105;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCAGCTGGTCTTTGGCATC 60
DB 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCAGCTGGTCTTTGGCATC 60
QY 61 GAGCTGATGGAAGTGGACCCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
DB 61 GAGCTGATGGAAGTGGACCCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
QY 121 TCCTACGATGGCTGCTGGTGACATCAGATCATGCCACGAGGCTTCCTGATAATC 180
DB 121 TCCTACGATGGCTGCTGGTGACATCAGATCATGCCACGAGGCTTCCTGATAATC 180
QY 181 ATCTTGGCCATATCGCAAGAGGCGGCGACTGTGCCCTGTAGGAG 225
DB 181 ATCTTGGCCATATCGCAAGAGGCGGCGACTGTGCCCTGTAGGAG 225

RESULT 3
ID AAX84122 standard; cDNA; 225 BP.
XX AC AAX84122;
XX DT 08-SEP-1999 (first entry)
XX DE MAGE-6 gene.
XX KW Tumour rejection antigen; vaccine; cancer; MAGE-6 gene; ss.
XX OS Homo sapiens.
XX PN US5925729-A.
XX PR 02-MAY-1994; 94US-0142368.
XX PR 02-MAY-1994; 94US-0142368.
XX PR 23-MAY-1991; 91US-0705702.
XX PR 09-JUL-1991; 91US-0728838.
XX PR 23-SEP-1991; 91US-0764365.
XX PR 12-DEC-1991; 91US-0807043.
XX PA (LUDW-) LUDWIG INST CANCER RES.

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XX Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
XX PI Van Den Eynde B, Van Der Bruggen P, Van Pel A;
XX DR WPI; 1999-418294/35.
XX PT New tumour rejection antigen is useful as a vaccine against
XX PT cancerous diseases
XX PS
XX Disclosure; Column 69-70; 58pp; English.
XX CC This sequence represents the MAGE-6 gene sequence.
XX CC The invention relates to a tumour rejection antigen sequence that is
XX CC useful as a tumour rejection antigen for vaccination against cancerous
XX CC conditions.
XX SQ
XX Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 20; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.le-105;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCAGCTGGTCTTTGGCATC 60
DB 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCAGCTGGTCTTTGGCATC 60
QY 61 GAGCTGATGGAAGTGGACCCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
DB 61 GAGCTGATGGAAGTGGACCCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
QY 121 TCCTACGATGGCTGCTGGTGACATCAGATCATGCCACGAGGCTTCCTGATAATC 180
DB 121 TCCTACGATGGCTGCTGGTGACATCAGATCATGCCACGAGGCTTCCTGATAATC 180
QY 181 ATCTTGGCCATATCGCAAGAGGCGGCGACTGTGCCCTGTAGGAG 225
DB 181 ATCTTGGCCATATCGCAAGAGGCGGCGACTGTGCCCTGTAGGAG 225

RESULT 4
ID AAT01166 standard; DNA; 225 BP.
XX AC AAT01166;
XX DT 26-FEB-1996 (first entry)
XX DE MAGE-6 gene.
XX KW MAGE-6; melanoma; tumour rejection antigen; cancer; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9523874-A1.
XX PR 30-NOV-1994; 94US-0346774.
XX PR 01-MAR-1994; 94US-0204727.
XX PR 10-MAR-1994; 94US-0209172.
XX PR 01-SEP-1994; 94US-0299849.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Boon-Falleur T, Brasseur F, Chomez P, De Plaen E;
XX PI De Smet C, Gaugler B, Lethe B, Marchand M, Patard J;
XX PI Szikora J, Van Den Eynde B, Van Derbruggen P, Weynants P;
XX DR WPI; 1995-320586/41.
XX

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	Query Match	69.9%	Score 157;	DB 20;	Length 1362;
	Best Local Similarity	100.0%;	Pred. No. 1.8e-70;		
	Matches 157;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
QY	4	TTCCTTCCGTGATCTTCAGCAAGCTTCGGATCTCCTTGACGTGGTCTTTGGCATCGAG	63		
Dd	826	tcttctcgtgatcttcagaaagcttcgattcccttgacgtggctttggcatcgag	885		
QY	64	CTGATGGAAGTGGACCCTCGGCCACGTGTACATCTTTGCACCTGCTGGGCTCTCC	123		
Dd	886	ctgatgaagtggaccacctgcgcccaogtatacatcttgcacactgcctgggcctccc			
QY	124	TACATGGCTGCTGGGTGCACAATFAGATCATGCCCA	160		
Dd	946	tacatagcctgctgggtgacaatcacatcatgccca	982		

New protein derivatives used in cancer vaccine therapy for treating a range of cancers including melanomas, carcinomas and cancers of

CC The present sequence represents a MAGE-6 cDNA encoding a human tumor  
CC rejection antigen (TRA) precursor. The invention provides for TRAs  
CC (AAW56268-W56272) which are processed from TRA precursors that are  
CC derived from the MAGE-6 gene. The TRAs bind to major histocompatibility  
CC complex (MHC) molecules of the type HLA-Cw\*16 to provoke a cytotoxic  
CC T-cell response against cells exhibiting this particular TRA-MHC  
CC complex. As the cells presenting these complexes are human cancerous  
CC cells, the TRA peptides are claimed to be useful in provoking lysis of  
CC these cancerous cells thereby providing a probable method of treating  
CC cancer.  
XX  
SQ Sequence 1375 BP; 293 A; 364 C; 404 G; 314 T; 0 other;

Query Match 69.8%; Score 157; DB 19; Length 1375;  
Best Local Similarity 100.0%; Pred. No. 1.8e-70;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 TCTCTTCCTGTCATCTTCAGCAAGCTTCGGATTCCTTGCGATCGTCTTTGGCATCGAG 63  
DB 595 tctcttcctgtgattcttcagcaagcttcgattccttcgagctgtgtcttggcatcgag 654  
QY 64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGGCACCTGCTGGGCCCTCTCC 123  
DB 655 ctgatggaagtggaccctcgccacgtgtacatctttgcccacctgctgggacctctcc 714  
QY 124 TACGATGGCTGCTGGGTGACATCAGATCATGCCCA 160  
DB 715 tacgatggcctgctgggtgacaatcagatcatgccca 751

RESULT 7  
AAS02056  
ID AAS02056 standard; cDNA; 4204 BP.  
XX  
AC AAS02056;  
XX  
DT 16-JUL-2001 (first entry)  
XX  
DE DNA encoding molecule for disease detection and treatment, mddt21.  
XX  
KW Human; mddt21; gene therapy; adenosine deaminase deficiency;  
KW ADA; severe combined immunodeficiency syndrome; cystic fibrosis;  
KW thalassemia; familial hypercholesterolemia; haemophilia; factor VIII;  
KW factor IX; cancer; cell proliferation; parasite; human retrovirus; HIV;  
KW hepatitis B; hepatitis C; Candida albicans; Plasmodium falciparum;  
KW Paracoccidioides brasiliensis; Trypanosoma brasiliensis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200123538-A2.  
XX  
PD 05-APR-2001.  
XX  
PF 22-SEP-2000; 2000WO-US26085.  
XX  
PR 28-SEP-1999; 99US-0156565.  
PR 30-NOV-1999; 99US-0168197.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Hodgson DM, Lincoln SE, Russo FD, Spiro PA, Banville SC;  
PI Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Shah P, Chalup MS;  
PI Hillman JL, Jones AL, Yu JY, Greenawalt LB, Panzer SR;  
PI Roseberry AM, Wright RJ, Chen W, Liu TF, Yap PE, Stockdreher TK;  
PI Amshey S, Fong WT;  
XX  
DR WPI; 2001-258131/26.  
XX  
PT Purified disease treatment and detection molecule polynucleotides and  
PT polypeptides, useful for providing diagnostic assays and gene therapy -  
XX  
PS Claim 1; Page 109-110; 113pp; English.

XX The sequence represents the coding sequence of molecule for disease  
CC detection and treatment, mddt21, shown by computer analysis to be similar  
CC to the MAGE family of proteins. The sequence may be used for  
CC somatic or germline gene therapy. Gene therapy may be performed to: (i)  
CC correct genetic deficiency such as in severe combined immunodeficiency  
CC syndrome associated with adenosine deaminase (ADA) deficiency, cystic  
CC fibrosis, thalassemias, familial hypercholesterolemia and haemophilia  
CC caused by factor VIII or factor IX deficiencies; (ii) express a  
CC conditional lethal gene product (such as in the case of cancers which  
CC result from unregulated cell proliferation); (iii) express a protein  
CC which affords protection against intracellular parasites (for example,  
CC human retroviruses such as HIV, hepatitis B or C, fungal parasites such  
CC as Candida albicans and Paracoccidioides brasiliensis, and protozoal  
CC parasites such as Plasmodium falciparum and Trypanosoma brasiliensis.  
XX  
SQ Sequence 4204 BP; 947 A; 1145 C; 1219 G; 893 T; 0 other;

Query Match 69.8%; Score 157; DB 22; Length 4204;  
Best Local Similarity 100.0%; Pred. No. 1.9e-70;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 TCTCTTCCTGTCATCTTCAGCAAGCTTCGGATTCCTTGCGATCGTCTTTGGCATCGAG 63  
DB 2900 tctcttcctgtgattcttcagcaagcttcgattccttcgagctgtgtcttggcatcgag 2959  
QY 64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGGCACCTGCTGGGCCCTCTCC 123  
DB 2960 ctgatggaagtggaccctcgccacgtgtacatctttgcccacctgctgggacctctcc 3019  
QY 124 TACGATGGCTGCTGGGTGACATCAGATCATGCCCA 160  
DB 3020 tacgatggcctgctgggtgacaatcagatcatgccca 3056

RESULT 8  
AAD18141  
ID AAD18141 standard; cDNA; 666 BP.  
XX  
AC AAD18141;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Human melanoma associated antigen 3 (MAGE-3) truncated cDNA.  
XX  
KW Human; melanoma associated antigen 3; MAGE-3; neuroprotective; nootropic;  
KW immunosuppressive; caspase-12 activation; cell death related disease;  
KW cell death inhibitor; cancer-specific protein; Alzheimer's disease;  
KW neurodegenerative disease; autoimmune disease; amyotrophy; gene therapy;  
KW organ disorder; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..666  
FT /tag= a  
FT /product= "Human MAGE-3 protein"  
FT /note= "CDS does not include start codon"  
FT /partial  
XX  
PN EP1126027-A1.  
XX  
XX 22-AUG-2001.  
PD  
PD 16-FEB-2001; 2001EP-0301361.  
PF  
XX 18-FEB-2000; 2000JP-0041927.  
PR  
XX (RIKE ) RIKEN KK.  
XX  
PI Morishima N, Shibata T;  
XX

DR WPI: 2001-591501/67.  
XX P-PSDB; AAE10673.  
PT New polypeptide for treating cell death related diseases such as  
PT Alzheimer's disease, neurodegenerative diseases, autoimmune diseases,  
PT anyotrophy and organ disorders comprises the recombinant  
PT cancer-specific protein MAGE-3  
XX  
XX Claim 3; Page 25-27; 41pp; English.  
XX The present sequence is the truncated form of human melanoma  
CC associated antigen 3 (MAGE-3) cDNA. The present invention relates  
CC to MAGE-3 protein or its truncated form which specifically bind to  
CC caspase-12 or pro-caspase-12 protein and inhibit their activation.  
CC MAGE-3 proteins are cancer-specific proteins and are used as cell-  
CC death inhibitors. Therapeutic agents comprising MAGE-3 sequence are  
CC useful for treating cell death related diseases such as Alzheimer's  
CC disease, neurodegenerative diseases, autoimmune diseases, amyotrophy  
CC and organ disorders. MAGE-3 gene is useful as an agent for gene therapy.  
CC The sequences of the invention are useful for preventing or treating a  
CC cell death-related disease developing in tissues in the nervous system,  
CC vascular system, respiratory system, digestive system, lymph system,  
CC urinary system, or reproductive system.  
XX  
SQ Sequence 666 BP; 151 A; 165 C; 197 G; 153 T; 0 other;  
  
Query Match 32.9%; Score 74; DB 22; Length 666;  
Best Local Similarity 99.2%; Pred. No. 4.8e-28;  
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 36 TTCCTTGGCAGCTGCTTTGGCATCCAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95  
Db 189 ttctttgcagctggtctttggcatcgagctgatggaagtggaccatcgccacttgta 248  
  
QY 96 CATCTTTGGCAGCTGCTGCTGCTCTCTACGATGCGCTGCTGGGTGACAATCAGATCAT 155  
Db 249 catctttgccacctgctggcctctctctacatgagctgctgctgggtgacaatcagatcat 308  
  
QY 156 GCCCA 160  
Db 309 gccca 313  
  
RESULT 9  
AAD12993  
ID AAD12993 standard; DNA; 945 BP.  
XX  
AC AAD12993;  
DT 16-OCT-2001 (first entry)  
XX  
DE Human MAGE-A3 DNA.  
XX  
KW MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44;  
KW tumour cell; immunostimulant; antigen presentation; cancer; melanoma;  
KW CD8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma;  
KW myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic;  
KW gene therapy; human; MAGE-A3; tumour rejection antigen; TRA; ds.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 1. 945  
FT CDS  
FT /\*tag= a  
FT /product= "MAGE-A3 protein"  
XX  
XX WO200153833-A1.  
PN  
XX  
PD 26-JUL-2001.  
XX  
XX 19-JAN-2001; 2001WO-US02008.  
XX

PR 20-JAN-2000; 2000US-0177242.  
PR 25-OCT-2000; 2000US-0243212.  
XX  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX  
XX Luiten R, Boon-Falleur T, Van Der Bruggen P, Stroobant V;  
PI Demotte N, Schultz E;  
XX  
XX WPI: 2001-488724/53.  
DR P-PSDB; AAE06853.  
XX  
XX Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or  
PT HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used  
PT in diagnosis and treatment of a disorder characterized by expression of  
PT MAGE-A1 or -A3  
XX  
XX Example 3; Page 94-95; 103pp; English.  
XX The invention relates to functional variants and isolated mimetics of a  
CC MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide,  
CC or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described  
CC in the specification. MAGE genes encode tumour rejection antigens  
CC (TRAs) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules.  
CC The MAGE antigenic peptide acts by binding to HLA molecules  
CC on tumour cells and stimulating recognition of these cells and thus  
CC signalling them to the immune system for destruction. The peptide when  
CC presented by HLA molecule induces the activation and stimulation of  
CC CD8+ cytotoxic T lymphocytes. The MAGE antigenic peptide is used to  
CC treat and diagnose disorders characterised by expression of MAGE-A1  
CC or -A3. Disorders include cancers e.g melanomas, oesophageal, lung,  
CC head and neck, breast, colorectal, prostate, renal, bladder,  
CC hepatocellular, papillary thyroid and gastric carcinomas, myelomas,  
CC brain tumours, sarcomas, seminomas, and ovarian tumours. The present  
CC sequence is human MAGE-A3 DNA.  
XX  
SQ Sequence 945 BP; 210 A; 254 C; 278 G; 203 T; 0 other;  
  
Query Match 32.9%; Score 74; DB 22; Length 945;  
Best Local Similarity 99.2%; Pred. No. 4.9e-28;  
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 36 TTCCTTGGCAGCTGCTTTGGCATCCAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95  
Db 468 ttctttgcagctggtctttggcatcgagctgatggaagtggaccatcgccacttgta 527  
  
QY 96 CATCTTTGGCAGCTGCTGCTGCTCTCTACGATGCGCTGCTGGGTGACAATCAGATCAT 155  
Db 528 catctttgccacctgctggcctctctctacatgagctgctgctgggtgacaatcagatcat 587  
  
QY 156 GCCCA 160  
Db 588 gccca 592  
  
RESULT 10  
AAX87592  
ID AAX87592 standard; cDNA; 1212 BP.  
XX  
AC AAX87592;  
XX  
XX 26-OCT-1999 (first entry)  
DT  
XX Haemagglutinin-MAGE-3-His fusion DNA.  
DE  
DE MAGE-3; haemagglutinin; NSI-MAGE-3-His; fusion protein; tumour;  
KW melanoma; breast cancer; bladder cancer; lung cancer;  
KW head and squamous cell carcinoma; colon cancer;  
KW oesophagus carcinoma; vaccine; human; ss.  
XX  
XX Chimeric - Influenza virus.  
OS  
XX Chimeric - Homo sapiens.  
OS  
XX Chimeric - synthetic.

```
XX WO940188-A2.
PN 12-AUG-1999.
PD 02-FEB-1999; 99WO-EP00660.
PF 06-FEB-1998; 98GB-0002650.
PR 05-FEB-1998; 98GB-0002543.
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
PI WPI; 1999-494293/41.
XX P-PSDB; AAY06591.
XX New protein derivatives used in cancer vaccine therapy for treating
PT a range of cancers including melanomas, carcinomas and cancers of
PT breast
XX Example 7; Page 69; 72pp; English.
XX This DNA sequence codes for a fusion protein (see AAY06591) composed
CC of haemagglutinin NSI of influenza virus, the human MAGE-3
CC tumour-associated antigen and a hexahistidine tail. A vector
CC designed for recombinant expression of the fusion protein is
CC provided. MAGE-3 cDNA was amplified using primers that altered the
CC first 5 codons to Escherichia coli codon usage. The NSI moiety
CC provided the fusion protein with additional exogenous T-helper
CC epitopes. The invention relates to MAGE proteins fused to an
CC immunological fusion partner, e.g. NSI-MAGE-3-His. These novel
CC fusion proteins provide vaccines for immunotherapy of melanomas or
CC other MAGE-associated tumours like breast, bladder, lung and
CC non-small cell lung cancer, head and squamous cell carcinoma, colon
CC carcinoma and oesophagus carcinoma.
XX Sequence 1212 BP; 289 A; 319 C; 344 G; 260 T; 0 other;

Query Match 32.9%; Score 74; DB 20; Length 1212;
Best Local Similarity 99.2%; Pred. No. 4.9e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGGCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
Db 708 ttctctgcagctggtctttggcatcgagctgatggaagtggaacccatcgccacttgta 767

QY 96 CATCTTTGCCACCTGCTGGCCCTCTCTACGATGCGCTGCTGGTGACAAATCAGATCAT 155
Db 768 catctttgccacctgctggcctctctctacgatggcctgctgggtgacaatcagatcat 827

QY 156 GCCCA 160
Db 828 gccca 832

RESULT 11
AAX87588
ID AAX87588 standard; cDNA; 1353 BP.
XX AAX87588;
AC AAX87588;
XX 26-OCT-1999 (first entry)
XX Lipoprotein D-MAGE-3-His fusion DNA.
XX MAGE-3; lipoprotein D; LPD-MAGE-3-His; fusion protein; tumour;
KW melanoma; breast cancer; bladder cancer; lung cancer;
KW head and squamous cell carcinoma; colon cancer;
KW oesophagus carcinoma; vaccine; human; ss.
XX Chimeric - Haemophilus influenzae.
OS
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OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX WO940188-A2.
XX 12-AUG-1999.
XX 02-FEB-1999; 99WO-EP00660.
PF 06-FEB-1998; 98GB-0002650.
PR 05-FEB-1998; 98GB-0002543.
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
PI WPI; 1999-494293/41.
XX P-PSDB; AAY06589.
XX New protein derivatives used in cancer vaccine therapy for treating
PT a range of cancers including melanomas, carcinomas and cancers of
PT breast
XX Example 1; Page 66; 72pp; English.
XX This DNA sequence codes for a fusion protein (see AAY06589) composed
CC of lipidated protein D (LPD) of Haemophilus influenzae B, the human
CC MAGE-3 tumour-associated antigen and a hexahistidine tail. A
CC vector designed for recombinant expression of the fusion protein is
CC provided. MAGE-3 cDNA was amplified using primers that altered the
CC first 5 codons to Escherichia coli codon usage. The LPD moiety
CC provided the fusion protein with additional exogenous T-cell
CC epitopes and also increased expression levels in E. coli. The
CC lipid tail ensured optimal presentation of the antigen to
CC antigen-presenting cells. The affinity tag facilitated
CC purification. The invention relates to MAGE proteins fused to an
CC immunological fusion partner, e.g. LPD-MAGE-3-His. These novel
CC fusion proteins provide vaccines for immunotherapy of melanomas or
CC other MAGE-associated tumours like breast, bladder, lung and
CC non-small cell lung cancer, head and squamous cell carcinoma, colon
CC carcinoma and oesophagus carcinoma.
XX Sequence 1353 BP; 342 A; 337 C; 354 G; 320 T; 0 other;

Query Match 32.9%; Score 74; DB 20; Length 1353;
Best Local Similarity 99.2%; Pred. No. 4.9e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGGCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
Db 849 ttctctgcagctggtctttggcatcgagctgatggaagtggaacccatcgccacttgta 908

QY 96 CATCTTTGCCACCTGCTGGCCCTCTCTACGATGCGCTGCTGGTGACAAATCAGATCAT 155
Db 909 catctttgccacctgctggcctctctctacgatggcctgctgggtgacaatcagatcat 968

QY 156 GCCCA 160
Db 969 gccca 973

RESULT 12
AAQ72480
ID AAQ72480 standard; cDNA to mRNA; 1640 BP.
XX AAQ72480;
AC AAQ72480;
XX 22-JUN-1995 (first entry)
XX Tumour rejection antigen precursor MAGE-3 cDNA.
XX Tumour antigen rejection precursor; melanoma antigen-3; MAGE-3;
KW
```

KW cancer; cytolytic T cells; antigen D; human leucocyte antigen;  
 KW PIA gene; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 172..1116  
 FT /\*tag= a  
 PN WO9423031-A.  
 XX  
 XX  
 PD 13-OCT-1994.  
 XX  
 XX 17-MAR-1994; 94WO-US02877.  
 PF  
 XX 26-MAR-1993; 93US-0037230.  
 PR  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA  
 PI Boon-falleur T, Gaugier B, Van DEN EYNDE B, Van DER BRUGGEN P;  
 XX WPI; 1994-333192/41.  
 DR  
 XX  
 XX New tumour rejection antigen precursor MAGE3 - useful in  
 PT treatment and diagnosis of cancer  
 PT  
 XX Example 32; Page 64; 105pp; English.  
 PS  
 XX AAO72480 is the PIA gene fragment which contains the cDNA coding  
 CC sequence AAQ72470, which encodes melanoma antigen-3 (MAGE-3), a tumour  
 CC rejection antigen precursor. Melanomas characterised by the expression of  
 CC MAGE-3 can be detected, or monitored, by contacting a test sample with  
 CC an agent that can recognise MAGE-3. The melanoma can be treated by the  
 CC administration of cytolytic T cells specific for the complex of  
 CC antigen D (the mature rejection antigen derived from MAGE-3) and a  
 CC human leucocyte antigen (esp. HLA-A1).  
 XX  
 XX Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;  
 SQ

Query Match 32.9%; Score 74; DB 15; Length 1640;  
 Best Local Similarity 99.2%; Pred. No. 4.9e-28;  
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGCTTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 639 ttcttgcagctggtcttggcatcgagctgatggaagtggaccatcgccacttgta 698

QY 96 CATCTTTGCCACCTGCTGGGCTCTCTACGATGCTGCTGGTGACAAATCAGATCAT 155  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 699 catctttgccacctgctggcctctcctacgatgctgctgctgggtgacaatcagatcat 758

QY 156 GCCCA 160  
 |||||  
 Db 759 gccca 763

RESULT 13  
 AAX84116  
 ID AAX84116 standard; cDNA to mRNA; 1640 BP.  
 XX  
 AC AAX84116;  
 XX  
 XX 08-SEP-1999 (first entry)  
 DT  
 XX MAGE-3 gene.  
 DE  
 XX Tumour rejection antigen; vaccine; cancer; MAGE-3 gene; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX US925729-A.  
 PN  
 XX

PD 20-JUL-1999.  
 XX  
 PF 02-MAY-1994; 94US-0142368.  
 XX  
 XX 02-MAY-1994; 94US-0142368.  
 PR 23-MAY-1991; 91US-0705702.  
 PR 09-JUL-1991; 91US-0728838.  
 PR 23-SEP-1991; 91US-0764365.  
 PR 12-DEC-1991; 91US-0807043.  
 XX  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA  
 XX Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;  
 PI Van Den Eynde B, Van Der Bruggen P, Van Pel A;  
 XX WPI; 1999-418294/35.  
 DR  
 XX New tumour rejection antigen is useful as a vaccine against  
 PT cancerous diseases  
 PT  
 XX Disclosure; Column 51-54; 58pp; English.  
 PS  
 XX This sequence represents the MAGE-3 gene sequence.  
 CC The invention relates to a tumour rejection antigen sequence that is  
 CC useful as a tumour rejection antigen for vaccination against cancerous  
 CC conditions.  
 CC  
 XX Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;  
 SQ

Query Match 32.9%; Score 74; DB 20; Length 1640;  
 Best Local Similarity 99.2%; Pred. No. 4.9e-28;  
 Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGCTTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 639 ttcttgcagctggtcttggcatcgagctgatggaagtggaccatcgccacttgta 698

QY 96 CATCTTTGCCACCTGCTGGGCTCTCTACGATGCTGCTGGTGACAAATCAGATCAT 155  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 699 catctttgccacctgctggcctctcctacgatgctgctgctgggtgacaatcagatcat 758

QY 156 GCCCA 160  
 |||||  
 Db 759 gccca 763

RESULT 14  
 AAX26974  
 ID AAX26974 standard; cDNA; 4204 BP.  
 XX  
 AC AAX26974;  
 XX  
 DT 25-JUN-1999 (first entry)  
 DT  
 XX cDNA encoding MAGE-3 polypeptide.  
 DE  
 XX MAGE-3 tumour associated gene; human leucocyte antigen Class II;  
 KW autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;  
 KW osteosarcoma; leukemia; carcinoma; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH 2465..3409  
 FT /\*tag= a  
 FT /product= "MAGE-3"  
 FT  
 XX WO9914326-A1.  
 PN  
 XX 25-MAR-1999.  
 PD  
 XX 04-SEP-1998; 98WO-US18601.  
 PF



```
XX PR 12-SEP-1997; 97US-0928615.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (UYVR-) UNIV VRIJE BRUSSEL.
XX PI Boon-Falleur T, Chaux P, Corthals J, Heirman C;
XX PI Lulten R, Stroobant V, Thielemans K, Van Der Bruggen P;
XX DR WPI: 1999-244031/20.
XX DR P-PSDB; AAY01720.
XX PT Isolated peptides that bind to human leucocyte antigen class II
XX PT molecules
XX PS Example 5; Page 65-67; 88pp; English.
XX CC The present sequence represents the MAGE-3 tumour associated gene.
XX CC Peptides that bind human leucocyte antigen (HLA) class II molecules
XX CC can be derived from the MAGE-3 protein. These peptides and
XX CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide
XX CC and HLA Class II, are used to treat MAGE-3 related diseases,
XX CC particularly cancers (e.g. melanoma, osteosarcoma, leukemia and
XX CC various forms of carcinoma). The peptides are also used to produce
XX CC specific antibodies. Detection of of the peptides, e.g. in binding
XX CC assays, particularly with antibodies, is used for diagnosis of such
XX CC diseases.
XX SQ Sequence 4204 BP; 944 A; 1144 C; 1223 G; 893 T; 0 other;

Query Match 32.9%; Score 74; DB 20; Length 4204;
Best Local Similarity 99.2%; Pred. No. 5e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCCTTGACAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
DB 2932 ttccttgagctggcttttggcatcgagctgagctgagtggaagtggaaccccatcgccactgtga 2991

QY 96 CATCTTTGCCACCTGCTGGGCTCTCCCTACGATGGCCTGCTGGGTGACAAATCAGATCAT 155
DB 2992 catctttgacactgctggcctctcctcacgacgatggcctgctgggtgacaatcagatcat 3051

QY 156 GCCCA 160
DB 3052 gccca 3056

RESULT 15
AAA37927
ID AAA37927 standard; cDNA; 4204 BP.
AC AAA37927;
DT 18-AUG-2000 (first entry)
DE Human MAGE-A3 nucleotide sequence.
XX
KW MAGE-A3; HLA class II; human leucocyte antigen; antibody; vaccine;
KW cancer; human; tumour; tumour associated gene product; ss.
XX
OS Homo sapiens.
XX
PN WO200020581-A1.
XX
PD 13-APR-2000.
XX
PF 15-SEP-1999; 99WO-US21230.
XX
PR 05-OCT-1998; 98US-0166448.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYVR-) UNIV VRIJE BRUSSEL.
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XX PI Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;
XX PI Schultz ES, Van Snick J, Lethe B, Thielemans K, Corthals J;
XX PI Heirman C;
XX WPI: 2000-317713/27.
XX DR P-PSDB; AAB02565.
XX PT New MAGE-A3 class II binding peptides, useful to diagnose and treat
XX PT tumours, are fragments of MAGE-A3 which bind to and are presented to T
XX PT lymphocytes by human leucocyte antigen class II molecules.
XX PS Example 6; Page 96-98; 119pp; English.
XX CC The present invention relates to MAGE-A3 (tumour associated gene
XX CC product) human leucocyte antigen (HLA) class II-binding peptides (see
XX CC AAB02566-B02595, and AAB02633-B02637). These peptides are presented to T
XX CC cells in the context of HLA class II molecules. The peptides stimulate
XX CC the activity and proliferation of CD4+ T lymphocytes. The invention also
XX CC includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928
XX CC and AAA37938-A37940). The peptides and nucleotide sequences can be used
XX CC to create antibodies against the MAGE-A3 peptides, the antibodies,
XX CC peptides and nucleotide sequences can be used to create a vaccine. The
XX CC expression of MAGE-3, particularly cancer. The methods can also be used
XX CC in the diagnosis of disorders associated with MAGE-3 expression. Included
XX CC in the invention are other human tumour antigens (see AAB02596-B02637),
XX CC and PCR primers used in the course of the invention (see AAA37929-A37937
XX CC and AAA37941-A37942).
XX SQ Sequence 4204 BP; 944 A; 1144 C; 1223 G; 893 T; 0 other;

Query Match 32.9%; Score 74; DB 21; Length 4204;
Best Local Similarity 99.2%; Pred. No. 5e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCCTTGACAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
DB 2932 ttccttgagctggcttttggcatcgagctgagctgagtggaagtggaaccccatcgccactgtga 2991

QY 96 CATCTTTGCCACCTGCTGGGCTCTCCCTACGATGGCCTGCTGGGTGACAAATCAGATCAT 155
DB 2992 catctttgacactgctggcctctcctcacgacgatggcctgctgggtgacaatcagatcat 3051

QY 156 GCCCA 160
DB 3052 gccca 3056

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OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 02:30:46 ; Search time 63.45 Seconds  
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Title: US-08-037-230D-18

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	225	100.0	225	1	US-07-807-043B-15
2	225	100.0	225	1	US-08-299-849B-18
3	225	100.0	225	2	US-08-142-368A-18
4	225	100.0	225	3	US-08-967-727-18
5	225	100.0	225	4	US-08-037-230D-18
6	157	69.8	945	4	US-09-056-105-7
7	157	69.8	1019	4	US-09-056-105-13
8	157	69.8	1375	2	US-08-993-738A-2
9	157	69.8	1375	4	US-08-713-354C-2
10	74	32.9	1640	1	US-07-807-043B-11
11	74	32.9	1640	1	US-08-299-849B-11
12	74	32.9	1640	2	US-08-142-368A-11
13	74	32.9	1640	3	US-08-967-727-11
14	74	32.9	1640	4	US-08-037-230D-11
15	74	32.9	4204	2	US-08-928-615-1
16	74	32.9	4204	4	US-09-056-105-6
17	74	32.9	4204	4	US-09-166-448-1
18	36	16.0	4157	1	US-07-807-043B-9
19	36	16.0	4157	1	US-08-299-849B-9
20	36	16.0	4157	2	US-08-142-368A-9
21	36	16.0	4157	3	US-08-967-727-9
22	36	16.0	4157	4	US-08-037-230D-9
23	36	16.0	4559	4	US-09-056-105-5
24	27	12.0	27	1	US-07-938-334C-18
25	27	12.0	27	1	US-08-073-103A-9
26	27	12.0	27	1	US-08-443-341-9
27	27	12.0	27	3	US-08-354-679C-9

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29	27	12.0	27	5	PCT-US93-08157-9	Sequence 9, Appli
c 30	26	11.6	26	3	US-09-064-964-24	Sequence 24, Appl
c 31	24	10.7	24	1	US-08-299-849B-34	Sequence 34, Appl
c 32	24	10.7	24	2	US-09-018-423-10	Sequence 10, Appl
c 33	24	10.7	24	4	US-09-351-351-10	Sequence 10, Appl
c 34	24	10.7	24	4	US-09-183-931-10	Sequence 10, Appl
35	23	10.2	1084	2	US-08-184-009-110	Sequence 110, App
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43	23	10.2	2226	1	US-08-299-849B-16	Sequence 16, Appl
44	23	10.2	2226	2	US-08-142-368A-16	Sequence 16, Appl
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47	23	10.2	2305	1	US-08-299-849B-17	Sequence 17, Appl
48	23	10.2	2305	2	US-08-142-368A-17	Sequence 17, Appl
49	23	10.2	2305	3	US-08-967-727-17	Sequence 17, Appl
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52	23	10.2	2419	1	US-08-299-849B-7	Sequence 7, Appli
53	23	10.2	2419	3	US-08-142-368A-7	Sequence 7, Appli
54	23	10.2	2419	3	US-08-967-727-7	Sequence 7, Appli
55	23	10.2	2419	4	US-08-037-230D-7	Sequence 7, Appli
56	23	10.2	2420	1	US-08-465-167A-23	Sequence 23, Appl
57	23	10.2	2420	4	US-09-056-105-4	Sequence 4, Appli
58	23	10.2	4736	4	US-09-056-105-12	Sequence 12, Appl
59	23	10.2	4741	4	US-09-056-105-11	Sequence 11, Appl
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61	23	10.2	5674	1	US-08-190-411A-1	Sequence 1, Appli
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63	23	10.2	5674	2	US-08-560-024-1	Sequence 1, Appli
64	23	10.2	5674	2	US-08-142-368A-8	Sequence 8, Appli
65	23	10.2	5674	3	US-08-967-727-8	Sequence 8, Appli
66	23	10.2	5674	4	US-08-037-230D-8	Sequence 8, Appli
67	21	9.3	27	1	US-07-938-334C-13	Sequence 13, Appl
68	21	9.3	27	1	US-08-073-103A-4	Sequence 4, Appli
69	21	9.3	27	1	US-08-443-341-4	Sequence 4, Appli
70	21	9.3	27	3	US-08-354-679C-4	Sequence 4, Appli
71	21	9.3	27	4	US-08-393-273E-4	Sequence 4, Appli
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76	21	9.3	1810	4	US-08-037-230D-20	Sequence 20, Appl
77	21	9.3	3839	4	US-09-056-105-14	Sequence 14, Appl
78	18	8.0	4031	2	US-08-993-118-1	Sequence 1, Appli
79	18	8.0	4031	3	US-08-845-528C-1	Sequence 1, Appli
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c 83	17	7.6	930	4	US-09-227-357-61	Sequence 61, Appl
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85	17	7.6	1947	1	US-08-299-849B-19	Sequence 19, App
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88	17	7.6	1947	4	US-08-037-230D-19	Sequence 19, App
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93	16	7.1	54	4	US-09-235-375-3	Sequence 3, Appli
94	16	7.1	166	1	US-07-807-043B-16	Sequence 16, App
95	16	7.1	526	4	US-09-328-111-261	Sequence 261, App
c 96	16	7.1	635	4	US-09-328-111-56	Sequence 56, Appl
97	16	7.1	1022	4	US-09-056-105-8	Sequence 8, Appli
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102	16	7.1	1068	3	US-08-967-727-15	Sequence 15, Appl	c 175	15	6.7	10163	4	US-09-256-490-1	Sequence 1, Appl
103	16	7.1	1068	4	US-08-037-230D-15	Sequence 15, Appl	c 176	15	6.7	10163	5	PCT-US96-11445-1	Sequence 1, Appl
104	16	7.1	1412	1	US-08-299-849B-21	Sequence 21, Appl	c 177	15	6.7	36519	3	US-08-923-137-2	Sequence 2, Appl
105	16	7.1	1412	2	US-08-142-368A-21	Sequence 21, Appl	c 178	14	6.2	38	3	US-08-880-729-12	Sequence 12, Appl
106	16	7.1	1412	3	US-08-967-727-21	Sequence 21, Appl	c 179	14	6.2	50	1	US-08-620-467A-19	Sequence 19, Appl
107	16	7.1	1412	4	US-08-037-230D-21	Sequence 21, Appl	c 180	14	6.2	50	1	US-08-348-572-20	Sequence 20, Appl
108	16	7.1	1680	2	US-09-052-339-2	Sequence 20, Appl	c 181	14	6.2	50	3	US-09-041-090B-20	Sequence 20, Appl
109	16	7.1	1810	1	US-08-299-849B-20	Sequence 20, Appl	c 182	14	6.2	81	3	US-08-963-121C-10	Sequence 10, Appl
110	16	7.1	1810	2	US-08-142-368A-20	Sequence 20, Appl	c 183	14	6.2	81	4	US-09-543-513-10	Sequence 10, Appl
111	16	7.1	1810	3	US-08-967-727-20	Sequence 20, Appl	c 184	14	6.2	81	5	PCT-US95-04803-11	Sequence 11, Appl
112	16	7.1	1810	4	US-08-037-230D-20	Sequence 20, Appl	c 185	14	6.2	223	4	US-08-205-697A-14	Sequence 14, Appl
113	16	7.1	1826	2	US-09-052-339-3	Sequence 3, Appl	c 186	14	6.2	223	5	PCT-US95-02576-14	Sequence 14, Appl
114	16	7.1	2531	1	US-08-299-849B-13	Sequence 13, Appl	c 187	14	6.2	223	6	US-09-328-111-287	Sequence 11, Appl
115	16	7.1	2531	2	US-08-299-849B-14	Sequence 14, Appl	c 188	14	6.2	223	7	US-08-577-081A-2	Sequence 2, Appl
116	16	7.1	2531	3	US-08-142-368A-13	Sequence 13, Appl	c 189	14	6.2	242	3	US-08-577-081A-2	Sequence 2, Appl
117	16	7.1	2531	4	US-08-142-368A-14	Sequence 14, Appl	c 190	14	6.2	339	4	US-09-056-556-240	Sequence 240, App
118	16	7.1	2531	5	US-08-967-727-13	Sequence 13, Appl	c 191	14	6.2	530	2	US-08-757-036-2	Sequence 2, Appl
119	16	7.1	2531	6	US-08-967-727-14	Sequence 14, Appl	c 192	14	6.2	543	4	US-08-862-124-1	Sequence 1, Appl
120	16	7.1	2531	7	US-08-967-727-15	Sequence 15, Appl	c 193	14	6.2	543	4	US-08-862-124-3	Sequence 3, Appl
121	16	7.1	2531	8	US-08-037-230D-13	Sequence 13, Appl	c 194	14	6.2	633	4	US-09-230-637-2	Sequence 2, Appl
122	16	7.1	2531	9	US-08-037-230D-14	Sequence 14, Appl	c 195	14	6.2	633	4	US-09-328-111-475	Sequence 1, Appl
123	16	7.1	2774	3	US-08-466-548B-1	Sequence 1, Appl	c 196	14	6.2	687	1	US-08-403-388-4	Sequence 4, Appl
124	16	7.1	2774	4	PCT-US93-12560-1	Sequence 1, Appl	c 197	14	6.2	687	1	US-08-658-578-4	Sequence 4, Appl
125	16	7.1	2931	3	US-09-056-105-15	Sequence 15, Appl	c 198	14	6.2	687	3	US-08-846-111B-4	Sequence 4, Appl
126	16	7.1	3545	3	US-08-480-474-10	Sequence 10, Appl	c 199	14	6.2	693	4	US-09-187-789-8	Sequence 8, Appl
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128	16	7.1	4392	1	US-08-026-138E-5	Sequence 5, Appl	c 201	14	6.2	777	4	US-09-187-789-4	Sequence 4, Appl
129	16	7.1	4808	2	US-08-231-193A-10	Sequence 10, Appl	c 202	14	6.2	791	4	US-09-051-696-5	Sequence 5, Appl
130	16	7.1	4808	3	US-08-486-273A-10	Sequence 10, Appl	c 203	14	6.2	843	4	US-08-953-326-10	Sequence 10, Appl
131	16	7.1	4808	4	US-08-940-086A-10	Sequence 10, Appl	c 204	14	6.2	850	4	US-09-187-789-6	Sequence 6, Appl
132	16	7.1	4808	5	US-08-940-035A-10	Sequence 10, Appl	c 205	14	6.2	973	1	US-07-805-123C-8	Sequence 8, Appl
133	16	7.1	4858	3	US-08-436-332B-9	Sequence 9, Appl	c 206	14	6.2	973	3	US-08-033-081B-8	Sequence 8, Appl
134	16	7.1	4858	4	US-08-927-219-126	Sequence 126, App	c 207	14	6.2	973	3	US-09-013-881-16	Sequence 16, Appl
135	16	7.1	6254	4	US-09-056-105-9	Sequence 9, Appl	c 208	14	6.2	984	4	US-09-392-014-1	Sequence 1, Appl
136	16	7.1	11495	4	US-08-789-329C-11	Sequence 11, Appl	c 209	14	6.2	985	4	US-09-056-556-182	Sequence 182, App
137	15	6.7	129	4	US-08-789-329C-12	Sequence 12, Appl	c 210	14	6.2	1005	2	US-08-761-344-1	Sequence 1, Appl
138	15	6.7	138	4	US-08-998-416-852	Sequence 852, App	c 211	14	6.2	1017	4	US-08-793-634B-6	Sequence 6, Appl
139	15	6.7	716	3	US-09-188-930-33	Sequence 33, Appl	c 212	14	6.2	1062	4	US-09-067-800-1	Sequence 1, Appl
140	15	6.7	903	3	US-08-299-849B-22	Sequence 22, Appl	c 213	14	6.2	1062	4	US-09-105-652-1	Sequence 1, Appl
141	15	6.7	920	1	US-08-142-368A-22	Sequence 22, Appl	c 214	14	6.2	1062	4	US-09-349-677-1	Sequence 1, Appl
142	15	6.7	920	2	US-08-967-727-22	Sequence 22, Appl	c 215	14	6.2	1107	1	US-08-299-849B-23	Sequence 23, Appl
143	15	6.7	920	3	US-08-037-230D-22	Sequence 22, Appl	c 216	14	6.2	1107	2	US-08-142-368A-23	Sequence 23, Appl
144	15	6.7	1079	4	US-08-789-329C-6	Sequence 22, Appl	c 217	14	6.2	1107	3	US-08-967-727-23	Sequence 23, Appl
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152	15	6.7	2336	4	US-08-724-774B-3	Sequence 3, Appl	c 225	14	6.2	1414	2	US-08-476-976-62	Sequence 62, Appl
153	15	6.7	2559	3	US-09-089-595-3	Sequence 3, Appl	c 226	14	6.2	1414	3	US-08-474-410-62	Sequence 62, Appl
154	15	6.7	2559	4	US-09-382-855-3	Sequence 3, Appl	c 227	14	6.2	1414	4	US-08-486-673B-62	Sequence 62, Appl
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157	15	6.7	2574	3	US-09-256-490-13	Sequence 13, Appl	c 230	14	6.2	1796	2	US-09-269-040-4	Sequence 4, Appl
158	15	6.7	2574	4	PCT-US96-11445-13	Sequence 13, Appl	c 231	14	6.2	1796	2	US-08-911-445-17	Sequence 17, Appl
159	15	6.7	3510	4	US-09-056-105-16	Sequence 16, Appl	c 232	14	6.2	1796	4	US-09-182-983-17	Sequence 17, Appl
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165	15	6.7	6645	5	US-08-895-628-4	Sequence 4, Appl	c 238	14	6.2	1845	3	US-08-911-445-5	Sequence 5, Appl
166	15	6.7	8174	1	US-07-914-281-5	Sequence 5, Appl	c 239	14	6.2	1845	4	US-09-182-983-5	Sequence 5, Appl
167	15	6.7	8174	2	US-08-393-246-5	Sequence 5, Appl	c 240	14	6.2	1985	3	US-09-173-561-17	Sequence 17, Appl
168	15	6.7	8174	3	US-08-525-058A-5	Sequence 5, Appl	c 241	14	6.2	1985	4	US-09-420-915-17	Sequence 17, Appl
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170	15	6.7	8174	5	US-09-042-531-5	Sequence 5, Appl	c 243	14	6.2	2046	2	US-08-911-445-6	Sequence 6, Appl
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172	15	6.7	8409	5	US-09-167-681-37	Sequence 37, Appl	c 245	14	6.2	2074	2	US-09-018-576-2	Sequence 2, Appl
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396	13	5.8	373	2	US-08-083-741-3	Sequence 3, Appli	469	13	5.8	1119	1	US-08-416-756A-1	Sequence 1, Appli
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c 412	13	5.8	558	4	US-09-420-528-43	Sequence 43, Appl	c 485	13	5.8	1261	3	US-08-475-742-16	Sequence 16, Appl
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c 414	13	5.8	576	1	US-08-453-956-16	Sequence 16, Appl	c 487	13	5.8	1314	4	US-08-800-682-1	Sequence 1, Appli
c 415	13	5.8	576	1	US-08-086-631-16	Sequence 16, Appl	c 488	13	5.8	1331	4	US-08-944-604-17	Sequence 17, Appl
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c 418	13	5.8	593	4	US-09-328-111-724	Sequence 724, App	c 491	13	5.8	1361	2	US-08-909-119-4	Sequence 4, Appli
c 419	13	5.8	595	4	US-08-998-416-32	Sequence 32, Appl	c 492	13	5.8	1386	2	US-08-687-080-76	Sequence 76, Appl
c 420	13	5.8	598	4	US-09-328-111-291	Sequence 291, App	c 493	13	5.8	1389	1	US-08-702-344-20	Sequence 20, Appl
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c 422	13	5.8	607	3	US-09-188-930-236	Sequence 236, App	c 495	13	5.8	1413	4	US-09-031-962B-14	Sequence 14, Appl
c 423	13	5.8	625	4	US-09-328-111-205	Sequence 205, App	c 496	13	5.8	1460	2	US-08-933-750C-60	Sequence 60, Appl
c 424	13	5.8	632	4	US-09-328-111-444	Sequence 444, App	c 497	13	5.8	1460	3	US-09-234-613-60	Sequence 1, Appli
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c 428	13	5.8	675	4	US-09-220-528-27	Sequence 27, Appl	c 501	13	5.8	1491	4	US-09-082-092-9	Sequence 9, Appli
c 429	13	5.8	675	4	US-09-220-528-28	Sequence 28, Appl	c 502	13	5.8	1498	4	US-09-608-285A-45	Sequence 45, Appl
c 430	13	5.8	675	4	US-09-220-528-28	Sequence 28, Appl	c 503	13	5.8	1502	4	US-09-187-946-2	Sequence 2, Appli
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c 432	13	5.8	690	4	US-09-199-637A-194	Sequence 194, App	c 505	13	5.8	1551	4	US-08-943-731-70	Sequence 70, Appl
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c 693	13	5.8	2952	4	US-09-318-794A-4	Sequence 4, Appli	c 766	13	5.8	3808	2	US-08-609-230A-8	Sequence 8, Appli
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c 713	13	5.8	3164	1	US-08-188-228-49	Sequence 49, Appl	c 786	13	5.8	3941	4	US-08-401-632-21	Sequence 21, Appl
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c 745	13	5.8	3429	4	US-08-946-994-10	Sequence 10, Appl	c 818	13	5.8	4110	3	US-08-662-227-33	Sequence 33, Appl
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c 749	13	5.8	3479	4	US-09-265-315-7	Sequence 7, Appli	c 822	13	5.8	4138	2	US-08-447-411-75	Sequence 75, Appl
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c 839	13	5.8	4405	2	US-08-745-880-3	Sequence 3, Appli	c 912	13	5.8	8910	3	US-08-369-822C-19	Sequence 19, Appl
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c 844	13	5.8	4588	3	US-08-840-082-1	Sequence 1, Appli	c 917	13	5.8	9030	2	US-08-384-616-13	Sequence 13, Appl
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c 888	13	5.8	7298	2	US-08-710-637-3	Sequence 3, Appli	c 961	13	5.8	19877	3	US-09-079-587-8	Sequence 8, Appli
c 889	13	5.8	7298	2	US-08-194-468-1	Sequence 1, Appli	c 962	13	5.8	20303	1	US-08-370-975B-6	Sequence 6, Appli
c 890	13	5.8	7326	1	US-08-961-739-1	Sequence 1, Appli	c 963	13	5.8	21126	1	US-08-008-216-19	Sequence 19, Appl
c 891	13	5.8	7344	3	US-08-815-809-6	Sequence 1, Appli	c 964	13	5.8	21126	1	US-08-458-831-19	Sequence 19, Appl
892	13	5.8	7622	4	US-09-305-639-1	Sequence 6, Appli	c 965	13	5.8	26764	1	US-08-370-975B-1	Sequence 1, Appli
893	13	5.8	7797	2	US-08-816-155B-7	Sequence 7, Appli	c 966	13	5.8	28720	4	US-09-341-587-7	Sequence 7, Appli
894	13	5.8	7797	3	US-09-079-587-7	Sequence 7, Appli	c 967	13	5.8	31571	1	US-08-323-443B-1	Sequence 1, Appli
895	13	5.8	7824	1	US-08-718-388-6	Sequence 6, Appli	c 968	13	5.8	34446	4	US-09-103-330-35	Sequence 35, Appl
896	13	5.8	7863	2	US-08-324-977-35	Sequence 35, Appl	c 969	13	5.8	38682	4	US-08-943-731-2	Sequence 2, Appli
897	13	5.8	7863	2	US-08-384-616-35	Sequence 35, Appl	c 970	13	5.8	42235	4	US-09-193-637A-1	Sequence 1, Appli
898	13	5.8	7863	2	US-08-904-686A-35	Sequence 35, Appl	c 971	13	5.8	42395	3	US-08-742-105-101	Sequence 101, App
899	13	5.8	7863	2	US-09-315-850-35	Sequence 35, Appl	c 972	13	5.8	49136	4	US-09-422-869-1	Sequence 1, Appli
c 900	13	5.8	7863	4	US-08-984-709A-49	Sequence 49, Appl	c 973	13	5.8	49136	4	US-09-422-869-1	Sequence 1, Appli
c 901	13	5.8	7898	4	US-08-324-977-31	Sequence 31, Appl	c 974	13	5.8	50341	2	US-08-247-901C-1	Sequence 1, Appli
c 902	13	5.8	7917	1	US-08-384-616-31	Sequence 31, Appl	c 975	13	5.8	50341	2	US-09-075-904-1	Sequence 1, Appli
903	13	5.8	7917	2	US-08-384-616-31	Sequence 31, Appl	c 976	13	5.8	50937	4	US-09-428-517-1	Sequence 1, Appli

C 977 13 5.8 52297 4 US-09-426-436-1 Sequence 1, Appli  
C 978 13 5.8 52297 4 US-08-705-557-1 Sequence 1, Appli  
C 979 13 5.8 53526 3 US-08-658-136-2 Sequence 2, Appli  
C 980 13 5.8 53577 2 US-08-658-136-1 Sequence 1, Appli  
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C 985 13 5.8 56520 4 US-09-218-207-179 Sequence 179, App  
C 986 13 5.8 59065 4 US-09-813-817-3 Sequence 3, Appli  
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C 989 13 5.8 152331 3 US-09-128-155-16 Sequence 16, Appli  
C 990 13 5.8 176373 3 US-09-128-155-17 Sequence 17, Appli  
C 991 13 5.8 246240 2 US-08-724-394A-20 Sequence 20, Appli  
C 992 13 5.8 246240 2 US-08-724-394A-21 Sequence 21, Appli  
C 993 13 5.8 246240 2 US-08-724-394A-22 Sequence 22, Appli  
C 994 13 5.8 4411529 4 US-09-103-840A-1 Sequence 1, Appli  
C 995 12 5.3 15 1 US-08-122-433-43 Sequence 43, Appli  
C 996 12 5.3 17 3 US-08-973-273-19 Sequence 19, Appli  
C 997 12 5.3 17 4 US-08-584-040-2044 Sequence 2044, Ap  
C 998 12 5.3 17 4 US-08-584-040-4055 Sequence 4055, Ap  
C 999 12 5.3 18 4 US-08-584-040-3031 Sequence 3031, Ap  
1000 12 5.3 20 1 US-08-260-515-14 Sequence 14, Appli

## ALIGNMENTS

RESULT 1  
US-07-807-043B-15  
; Sequence 15, Application US/07807043B  
; Patent No. 5342774  
; GENERAL INFORMATION:  
; APPLICANT: Boon, Thierry, Van den Eynde, Beno t  
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor  
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/807,043B  
; FILING DATE: 19911212  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 424  
; FILING DATE: 23-SEPTEMBER-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/728,838  
; FILING DATE: 9-JULY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/705,702  
; FILING DATE: 23-May-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hanson, No. 5342774man D.  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD 253.3  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 225 base pairs  
; TYPE: NUCLEIC ACID

RESULT 2  
US-08-299-849B-18  
; Sequence 18, Application US/08299849B  
; Patent No. 5612201  
; GENERAL INFORMATION:  
; APPLICANT: De Plaen, Etienne; Boon-Palleur, Thierry;  
; APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;  
; APPLICANT: Chomez, Patrick  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In  
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/299,849B  
; FILING DATE: 1-SEPTEMBER-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/037,230  
; FILING DATE: 26-MARCH-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/04354  
; FILING DATE: 22-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/807,043  
; FILING DATE: 12-DECEMBER-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/764,364  
; FILING DATE: 23-SEPTEMBER-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/728,838  
; FILING DATE: 9-JULY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/705,702  
; FILING DATE: 23-May-1991

STRANDEDNESS: singular  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: MAGE-6 gene  
US-07-807-043B-15

Query Match 100.0%; Score 225; DB 1; Length 225;  
Best Local Similarity 100.0%; Pred. No. 4.5e-103;  
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TATTCTTTCCCTGCTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATC 60  
QY 61 GAGCTGATGAAGTGGACCCCATCGGCCACGCTGATATCTTTGCCACCTGCCTGGGCCCTC 120  
Db 61 GAGCTGATGAAGTGGACCCCATCGGCCACGCTGATATCTTTGCCACCTGCCTGGGCCCTC 120  
QY 121 TCCTAGATGGCTGCTGGTGACATCAGATCATGCCAGGACAGGCTTCCTGTATAATC 180  
Db 121 TCCTAGATGGCTGCTGGTGACATCAGATCATGCCAGGACAGGCTTCCTGTATAATC 180  
QY 181 ATCCTGGCCATATCGCAAGAGAGGGCGGACTGTGCCCTGAGGAG 225  
Db 181 ATCCTGGCCATATCGCAAGAGAGGGCGGACTGTGCCCTGAGGAG 225

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/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hanson, No. 5612201man D.
/ REGISTRATION NUMBER: 30,946
/ REFERENCE/DOCKET NUMBER: LUD 5355
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 688-9200
/ TELEFAX: (212) 838-3884
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 225 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: MAGE-6 gene
/ US-08-299-849B-18

Query Match          100.0%; Score 225; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.5e-103;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TATTCTTTCTCTGATCTTCAGCAAGCTTCGGATTCTCTTCGAGCTGGTCTTTGGCATC 60

QY 61 GAGCTGATGGAAGTGAACCCATCGGCCAGCGTGATCATCTTTGCCACCTGCGCTGGGCCTC 120
DB 61 GAGCTGATGGAAGTGAACCCATCGGCCAGCGTGATCATCTTTGCCACCTGCGCTGGGCCTC 120

QY 121 TCCTACGATGGCTGCTGGGTGACATCATGCCAGGACAGCGTTCCTGATAATC 180
DB 121 TCCTACGATGGCTGCTGGGTGACATCATGCCAGGACAGCGTTCCTGATAATC 180

QY 181 ATCCTGGCCATATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
DB 181 ATCCTGGCCATATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225

RESULT 3
US-08-142-368A-18
/ Sequence 18, Application US/08142368A
/ Patent No. 5925729
/ GENERAL INFORMATION:
/ APPLICANT: Boon-Palleur, Thierry; Van der Bruggen, Thierry;
/ APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
/ APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
/ TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
/ TITLE OF INVENTION: Rejection Antigens and Uses Thereof
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Felfe & Lynch
/ STREET: 805 Third Avenue
/ CITY: New York City
/ STATE: New York
/ ZIP: 10022
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: Wordperfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/142,368A
/ FILING DATE: 02-MAY-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/04354
/ FILING DATE: 22-MAY-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/807,043
/ FILING DATE: 12-DECEMBER-1991
/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: 07/764,364
/ FILING DATE: 23-SEPTEMBER-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/728,838
/ APPLICATION NUMBER: 9-JULY-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/705,702
/ FILING DATE: 23-May-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hanson, No. 5925729man D.
/ REGISTRATION NUMBER: 30,946
/ REFERENCE/DOCKET NUMBER: LUD 5253.4-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 688-9200
/ TELEFAX: (212) 838-3884
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 225 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: MAGE-6 gene
/ US-08-142-368A-18

Query Match          100.0%; Score 225; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.5e-103;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTCTTTCTCTGATCTTCAGCAAGCTTCGGATTCTCTTCGAGCTGGTCTTTGGCATC 60
DB 1 TATTCTTTCTCTGATCTTCAGCAAGCTTCGGATTCTCTTCGAGCTGGTCTTTGGCATC 60

QY 61 GAGCTGATGGAAGTGAACCCATCGGCCAGCGTGATCATCTTTGCCACCTGCGCTGGGCCTC 120
DB 61 GAGCTGATGGAAGTGAACCCATCGGCCAGCGTGATCATCTTTGCCACCTGCGCTGGGCCTC 120

QY 121 TCCTACGATGGCTGCTGGGTGACATCATGCCAGGACAGCGTTCCTGATAATC 180
DB 121 TCCTACGATGGCTGCTGGGTGACATCATGCCAGGACAGCGTTCCTGATAATC 180

QY 181 ATCCTGGCCATATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
DB 181 ATCCTGGCCATATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225

RESULT 4
US-08-967-727-18
/ Sequence 18, Application US/08967727
/ Patent No. 6025474
/ GENERAL INFORMATION:
/ APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
/ APPLICANT: van der Bruggen, Pierre; Boon-Palleur, Thierry
/ TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
/ TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Felfe & Lynch
/ STREET: 805 Third Avenue
/ CITY: New York City
/ STATE: New York
/ ZIP: 10022
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: Wordperfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/967,727
/ FILING DATE:
/ CLASSIFICATION: 435
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;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/037,230  
;; FILING DATE: 26-MARCH-1993  
;; APPLICATION NUMBER: PCT/US92/04354  
;; FILING DATE: 22-MAY-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/807,043  
;; FILING DATE: 12-DECEMBER-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/764,365  
;; FILING DATE: 23-SEPTEMBER-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/728,838  
;; FILING DATE: 9-JULY-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/705,702  
;; FILING DATE: 23-MAY-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Hanson, No. 6025474man D.  
;; REGISTRATION NUMBER: 30,946  
;; REFERENCE/DOCKET NUMBER: LUD 5353  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 688-9200  
;; TELEFAX: (212) 838-3884  
;; INFORMATION FOR SEQ ID NO: 18:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 225 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; FEATURE:  
;; NAME/KEY: MAGE-6 gene  
US-08-967-727-18

Query Match 100.0%; Score 225; DB 3; Length 225;  
Best Local Similarity 100.0%; Pred. No. 4.5e-103;  
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 TATTCTTCTTCGTGATCTTCAGCAAGCTTCGATTCTCGAGCTGGTCTTTGGCATC 60  
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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGGCCCTC 120  
|||||  
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGGCCCTC 120  
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QY 121 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180  
|||||  
Db 121 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180  
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QY 181 ATCTGGCCATATCGCAAGAGAGGCGGACTGTGCCCTGAGGAG 225  
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Db 181 ATCTGGCCATATCGCAAGAGAGGCGGACTGTGCCCTGAGGAG 225  
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RESULT 5  
US-08-037-230D-18  
; Sequence 18, Application US/08037230D  
; Patent No. 6235525  
; GENERAL INFORMATION:  
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;  
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For  
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felle & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
;; COMPUTER: IBM  
;; OPERATING SYSTEM: PC-DOS  
;; SOFTWARE: Wordperfect  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/037,230D  
;; FILING DATE: 26-MARCH-1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US92/04354  
;; FILING DATE: 22-MAY-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/807,043  
;; FILING DATE: 12-DECEMBER-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/764,364  
;; FILING DATE: 23-SEPTEMBER-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/728,838  
;; FILING DATE: 9-JULY-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/705,702  
;; FILING DATE: 23-MAY-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Hanson, No. 6235525man D.  
;; REGISTRATION NUMBER: 30,946  
;; REFERENCE/DOCKET NUMBER: LUD 5353  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 688-9200  
;; TELEFAX: (212) 838-3884  
;; INFORMATION FOR SEQ ID NO: 18:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 225 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; FEATURE:  
;; NAME/KEY: MAGE-6 gene  
US-08-037-230D-18

Query Match 100.0%; Score 225; DB 4; Length 225;  
Best Local Similarity 100.0%; Pred. No. 4.5e-103;  
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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|||||  
Db 1 TATTCTTCTTCGTGATCTTCAGCAAGCTTCGATTCTCGAGCTGGTCTTTGGCATC 60  
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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGGCCCTC 120  
|||||  
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGGCCCTC 120  
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QY 121 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180  
|||||  
Db 121 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180  
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QY 181 ATCTGGCCATATCGCAAGAGAGGCGGACTGTGCCCTGAGGAG 225  
|||||  
Db 181 ATCTGGCCATATCGCAAGAGAGGCGGACTGTGCCCTGAGGAG 225  
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RESULT 6  
US-09-056-105-7  
; Sequence 7, Application US/09056105  
; Patent No. 6287569  
; GENERAL INFORMATION:  
; APPLICANT: KIPPS, THOMAS J.  
; APPLICANT: WU, YUNCI  
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR  
; TITLE OF INVENTION: PROCESSING

; FILE REFERENCE: 233/221  
; CURRENT APPLICATION NUMBER: US/09/056,105  
; CURRENT FILING DATE: 1998-04-06  
; EARLIER APPLICATION NUMBER: 60/043,467  
; EARLIER FILING DATE: 1997-04-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 945  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-056-105-7

Query Match 69.8%; Score 157; DB 4; Length 945;

Best Local Similarity 100.0%; Pred. No. 2.9e-69;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 436 ttcttccctgtgattcttcgaaagcttcgcattccttgacgtgctcttggcatcgag 495  
|||||  
QY 64 CTGATGGAAGTGACCCCATCGCCACGTGTACATCTTTGCCACCTGGCCCTCTCC 123  
|||||  
DB 496 ctgatggaagtgaaccccatcgccacgtgtacattcttgccacctgctggcctctcc 555  
|||||  
QY 124 TAGCATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160  
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DB 556 tacgatggcctgctgggtgacaaatcagatcatgccca 592  
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## RESULT 7

US-09-056-105-13  
; Sequence 13, Application US/09056105  
; Patent No. 6287569  
; GENERAL INFORMATION:  
; APPLICANT: KIPPS, THOMAS J.  
; APPLICANT: WU, YUNQI  
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR  
; FILE REFERENCE: 233/221  
; CURRENT APPLICATION NUMBER: US/09/056,105  
; CURRENT FILING DATE: 1998-04-06  
; EARLIER APPLICATION NUMBER: 60/043,467  
; EARLIER FILING DATE: 1997-04-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 1019  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-056-105-13

Query Match 69.8%; Score 157; DB 4; Length 1019;

Best Local Similarity 100.0%; Pred. No. 2.9e-69;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 501 ttcttccctgtgattcttcgaaagcttcgcattccttgacgtgctcttggcatcgag 560  
|||||  
QY 64 CTGATGGAAGTGACCCCATCGCCACGTGTACATCTTTGCCACCTGGCCCTCTCC 123  
|||||  
DB 561 ctgatggaagtgaaccccatcgccacgtgtacattcttgccacctgctggcctctcc 620  
|||||  
QY 124 TAGCATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160  
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## RESULT 8

US-08-993-738A-2

; Sequence 2, Application US/08993738A  
; Patent No. 5928938  
; GENERAL INFORMATION:  
; APPLICANT: van der Bruggen, Pierre; DePlaen Etienne;  
; APPLICANT: Boon-Falieur, Thierry  
; TITLE OF INVENTION: Isolated Peptides Which Complex With  
; TITLE OF INVENTION: HLA-Cw\*16 Molecules, and Uses Thereof  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski L.L.P.  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/993,738A  
FILING DATE: 19-December-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/713,354  
FILING DATE: 13-September-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5928938man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5460.1 DIV - JEL/NDH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1375 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-993-738A-2

Query Match 69.8%; Score 157; DB 2; Length 1375;

Best Local Similarity 100.0%; Pred. No. 2.9e-69;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCCCTGTCATCTTCAGCAAGCTTCGGATTCTTCAGCTGGTCTTTGGCATCGAG 63  
|||||  
DB 595 TTCTTTCCCTGTCATCTTCAGCAAGCTTCGGATTCTTCAGCTGGTCTTTGGCATCGAG 654  
|||||  
QY 64 CTGATGGAAGTGACCCCATCGCCACGTGTACATCTTTGCCACCTGGCCCTCTCC 123  
|||||  
DB 655 CTGATGGAAGTGACCCCATCGCCACGTGTACATCTTTGCCACCTGGCCCTCTCC 714  
|||||  
QY 124 TAGCATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160  
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DB 715 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 751  
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## RESULT 9

US-08-713-354C-2  
; Sequence 2, Application US/08713354C  
; Patent No. 6265215  
; GENERAL INFORMATION:  
; APPLICANT: van der Bruggen, Pierre; DePlaen Etienne;  
; APPLICANT: Boon-Falieur, Thierry  
; TITLE OF INVENTION: Isolated Peptides Which Complex With  
; TITLE OF INVENTION: HLA-Cw\*16 Molecules, and Uses Thereof  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felte & Lynch

STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/713.354C  
FILING DATE: 13-September-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6265215man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5460  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1375 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-713-354C-2

Query Match 69.8%; Score 157; DB 4; Length 1375;  
Best Local Similarity 100.08; Pred. No. 2.9e-69;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTCCGATTCCTTCAGCTGTCTTTGGCATCGAG 63  
Db TTTCTTTCTGTGATCTTCAGCAAGCTCCGATTCCTTCAGCTGTCTTTGGCATCGAG 654  
QY 64 CTGATGGAAGTGGACCCACGCGACGTGTACATCTTTGCCACCTGCGGCGCTCTCC 123  
Db TTTCTTTCTGTGATCTTCAGCAAGCTCCGATTCCTTCAGCTGTCTTTGGCATCGAG 654  
QY 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160  
Db TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 751

RESULT 10  
US-07-807-043B-11  
Sequence 11, Application US/07807043B  
Patent No. 5342774

GENERAL INFORMATION:  
APPLICANT: Boon, Thierry, Van den Eynde, Beno t  
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor  
TITLE OF INVENTION: Rejection Antigens and Uses Thereof  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/807.043B  
FILING DATE: 19911212  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/764, 364  
FILING DATE: 23-SEPTEMBER-1991

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/728, 838  
FILING DATE: 9-JULY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/705, 702  
FILING DATE: 23-May-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5342774man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 253.3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1640 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: singular  
TOPOLOGY: linear  
MOLECULE TYPE: cdna to mrna  
FEATURE:  
NAME/KEY: CDNA MAGE-3  
US-07-807-043B-11

Query Match 32.9%; Score 74; DB 1; Length 1640;  
Best Local Similarity 99.2%; Pred. No. 5.4e-28;  
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGACGTGGTCTTTGGCATCGAGCTGATGGAGTGGACCCCATCGGCACGTGTA 95  
Db TTTCTTTGGACGTGGTCTTTGGCATCGAGCTGATGGAGTGGACCCCATCGGCACGTGTA 698  
QY 96 CATCTTTGGACGTGGTCTTTGGCATCGAGCTGATGGAGTGGACCCCATCGGCACGTGTA 155  
Db CATCTTTGGACGTGGTCTTTGGCATCGAGCTGATGGAGTGGACCCCATCGGCACGTGTA 758  
QY 156 GCCCA 160  
Db TTTCTTTGGACGTGGTCTTTGGCATCGAGCTGATGGAGTGGACCCCATCGGCACGTGTA 758

RESULT 11  
US-08-299-849B-11  
Sequence 11, Application US/08299849B  
Patent No. 5612201  
GENERAL INFORMATION:  
APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;  
APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;  
APPLICANT: Chomez, Patrick  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In  
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/299.849B  
FILING DATE: 1-SEPTEMBER-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/037, 230  
FILING DATE: 26-MARCH-1993  
APPLICATION NUMBER: PCT/US92/04354

; FILING DATE: 22-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/807,043  
; FILING DATE: 12-DECEMBER-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/764,364  
; FILING DATE: 23-SEPTEMBER-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/728,838  
; FILING DATE: 23-MAY-1991  
; APPLICATION NUMBER: 07/705,702  
; FILING DATE: 23-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hanson, No. 5612201man D.  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD 5355  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1640 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; FEATURE:  
; NAME/KEY: cDNA MAGE-3  
US-08-299-849B-11

Query Match 32.9%; Score 74; DB 1; Length 1640;  
Best Local Similarity 99.2%; Pred. No. 5.4e-28;  
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCTTGCAGCTGGCTTTGGCATCGAGCTGATGGAGTGGACCCCATCGGCACGTGTA 95  
Db 639 TTCTTGCAGCTGGCTTTGGCATCGAGCTGATGGAGTGGACCCCATCGGCACGTGTA 698  
QY 96 CATCTTTGGCACCTGCTGGGCTCTCCCTACGATGGCTGCTGGGTGACAAATCAGATCAT 155  
Db 699 CATCTTTGGCACCTGCTGGGCTCTCCCTACGATGGCTGCTGGGTGACAAATCAGATCAT 758  
QY 156 GCCCA 160  
Db 759 GCCCA 763

RESULT 12  
US-08-142-368A-11  
; Sequence 11, Application US/08142368A  
; Patent No. 5925729  
; GENERAL INFORMATION:  
; APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;  
; APPLICANT: van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;  
; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia  
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor  
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/142,368A

; FILING DATE: 02-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/04354  
; FILING DATE: 22-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/807,043  
; FILING DATE: 12-DECEMBER-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/764,364  
; FILING DATE: 23-SEPTEMBER-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/728,838  
; FILING DATE: 23-MAY-1991  
; APPLICATION NUMBER: 07/705,702  
; FILING DATE: 23-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hanson, No. 5925729man D.  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD 5253.4-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1640 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; FEATURE:  
; NAME/KEY: cDNA MAGE-3  
US-08-142-368A-11

Query Match 32.9%; Score 74; DB 2; Length 1640;  
Best Local Similarity 99.2%; Pred. No. 5.4e-28;  
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCTTGCAGCTGGCTTTGGCATCGAGCTGATGGAGTGGACCCCATCGGCACGTGTA 95  
Db 639 TTCTTGCAGCTGGCTTTGGCATCGAGCTGATGGAGTGGACCCCATCGGCACGTGTA 698  
QY 96 CATCTTTGGCACCTGCTGGGCTCTCCCTACGATGGCTGCTGGGTGACAAATCAGATCAT 155  
Db 699 CATCTTTGGCACCTGCTGGGCTCTCCCTACGATGGCTGCTGGGTGACAAATCAGATCAT 758  
QY 156 GCCCA 160  
Db 759 GCCCA 763

RESULT 13  
US-08-967-727-11  
; Sequence 11, Application US/08967727  
; Patent No. 6025474  
; GENERAL INFORMATION:  
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;  
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For  
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
; COMPUTER: IBM  
; OPERATING SYSTEM: PC-DOS

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; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,727
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6025474man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1640 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; FEATURE:
; NAME/KEY: CDNA MAGE-3
;
US-08-967-727-11

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Query Match 32.9%; Score 74; DB 3; Length 1640;
Best Local Similarity 99.2%; Pred. No. 5.4e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
Db 639 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 698

QY 96 CATCTTTGCCACCTGCCTGGGCTCTCTACGATGCCCTGCTGGTGGTGAACAATCAGATCAT 155
Db 699 CATCTTTGCCACCTGCCTGGGCTCTCTACGATGCCCTGCTGGTGGTGAACAATCAGATCAT 758

QY 156 GCCCA 160
Db 759 GCCCA 763

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RESULT 14
US-08-037-230D-11
; Sequence 11, Application US/08037230D
; Patent No. 6235525
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor MAGE-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fefire & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York

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; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/037,230D
; FILING DATE: 26-MARCH-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6235525man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1640 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; FEATURE:
; NAME/KEY: CDNA MAGE-3
;
US-08-037-230D-11

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Query Match 32.9%; Score 74; DB 4; Length 1640;
Best Local Similarity 99.2%; Pred. No. 5.4e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
Db 639 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 698

QY 96 CATCTTTGCCACCTGCCTGGGCTCTCTACGATGCCCTGCTGGTGGTGAACAATCAGATCAT 155
Db 699 CATCTTTGCCACCTGCCTGGGCTCTCTACGATGCCCTGCTGGTGGTGAACAATCAGATCAT 758

QY 156 GCCCA 160
Db 759 GCCCA 763

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RESULT 15
US-08-928-615-1
; Sequence 1, Application US/08928615
; Patent No. 5965535
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED
; TITLE OF INVENTION: BY HLA CLASS II MOLECULES
; NUMBER OF SEQUENCES: 13

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Job time: 4446 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 01:34:31 ; Search time 2080.58 Seconds  
(without alignments)  
1459.600 Million cell updates/sec

Title: US-08-037-230D-18  
Perfect score: 225  
Sequence: 1 TATTCTTTCTGTGATCTT.....CCGACTGCGCCCTGAGGAG 225

Scoring table: OLIIGO\_NUC  
Gapop 60.0 , Gapext 60.0  
Searched: 13736207 seqs, 6748477542 residues

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Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
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Post-processing: Listing first 1000 summaries

- Database :
- 1: em\_estba.\*
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  - 6: em\_estpl.\*
  - 7: em\_estro.\*
  - 8: em\_htc.\*
  - 9: gb\_est1.\*
  - 10: gb\_est2.\*
  - 11: gb\_htc.\*
  - 12: gb\_gss.\*
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  - 15: em\_gss\_pln.\*
  - 16: em\_gss\_vrt.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	157	69.8	886	10	BG476078 602520963
6	157	69.8	894	10	BG765817 602739647
7	137	60.9	707	10	BG760839 602717006
8	137	60.9	876	10	BF792356 602252896
9	128	56.9	1021	10	BM470991 AGENCOURT
10	108	48.0	795	10	BE541476 601067928
11	104	46.2	696	10	BE733003 601569780
12	102	45.3	704	10	BG764972 602737745
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14	98	43.6	1101	10	BE734462 601566241
15	93	41.3	768	10	BG718421 602696451
16	93	41.3	929	10	BE275276 601122114
17	84	37.3	738	10	BE900916 601674359

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c 99	19	8.4	290	9	BB464671	BB464671	BB464671	c 172	17	7.6	277	9	AA516193	AA516193	RC2-ET002
c 100	19	8.4	336	10	BF924687	BF924687	IL5-NT023	c 173	17	7.6	279	9	AW946625	AW946625	RC2-ET002
c 101	19	8.4	624	10	BG522686	BG522686	24-27 Ste	c 174	17	7.6	287	10	TI9408	TI9408	h04001s Tes
c 102	19	8.4	719	12	AZ520448	AZ520448	RPC1-11-3	c 175	17	7.6	288	9	AW946628	AW946628	RC2-ET002
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c 104	19	8.4	808	10	BF238888	BF238888	601904516	c 177	17	7.6	289	10	R72779	R72779	yJ91f12.r1
c 105	19	8.4	1167	10	BE615120	BE615120	601280503	c 178	17	7.6	291	9	AA663202	AA663202	ab74e06.s
c 106	18	8.0	159	10	BF856493	BF856493	IL0-FT018	c 179	17	7.6	295	9	BB585473	BB585473	BB585473
c 107	18	8.0	194	12	AQ299332	AQ299332	HS-2219.A	c 180	17	7.6	296	10	BF772891	BF772891	IL5-IT002
c 108	18	8.0	256	10	T29724	T29724	ES922093.Hu	c 181	17	7.6	298	9	AW946665	AW946665	RC2-ET002
c 109	18	8.0	260	9	AV224480	AV224480	AV224480	c 182	17	7.6	299	9	AV091342	AV091342	AV091342
c 110	18	8.0	317	9	AW855322	AW855322	PM1-CT026	c 183	17	7.6	304	9	BB572064	BB572064	BB572064
c 111	18	8.0	345	10	BE924050	BE924050	EST427819	c 184	17	7.6	305	9	AA501450	AA501450	ne67f04.s
c 112	18	8.0	351	9	AW378888	AW378888	PM3-HT022	c 185	17	7.6	305	10	BF755080	BF755080	PM3-CT054
c 113	18	8.0	387	10	BF873525	BF873525	IL5-FT011	c 186	17	7.6	307	10	BG012627	BG012627	IL5-GN023
c 114	18	8.0	396	10	BF808408	BF808408	RC3-CI004	c 187	17	7.6	309	10	BE774144	BE774144	MRI-UM000
c 115	18	8.0	415	10	BE318532	BE318532	NF040B06L	c 188	17	7.6	311	10	BG011191	BG011191	IL5-GN023
c 116	18	8.0	464	9	AL372985	AL372985	MCBA54H12	c 189	17	7.6	313	9	AA559695	AA559695	MC031032
c 117	18	8.0	474	9	AW462799	AW462799	BF230010B	c 190	17	7.6	316	10	BG012624	BG012624	IL5-GN023
c 118	18	8.0	493	9	AV627486	AV627486	AV627486	c 191	17	7.6	324	10	BB862515	BB862515	UT-M-AL1-
c 119	18	8.0	497	10	BE921146	BE921146	EST424915	c 192	17	7.6	324	10	BB862515	BB862515	UT-M-AL1-
c 120	18	8.0	501	9	AW063136	AW063136	TN0280.KR	c 193	17	7.6	328	9	AA515733	AA515733	ng70f10.s
c 121	18	8.0	502	10	BF025153	BF025153	g910b02.x	c 194	17	7.6	330	10	BF599534	BF599534	263353.MA
c 122	18	8.0	510	9	AV643501	AV643501	AV643501	c 195	17	7.6	331	9	AA657420	AA657420	nt65c08.s
c 123	18	8.0	519	10	B1012485	B1012485	PM4-EN006	c 196	17	7.6	331	9	AA630911	AA630911	nt58g08.s
c 124	18	8.0	520	12	AQ251736	AQ251736	HS-3202.B	c 197	17	7.6	332	9	AA630910	AA630910	nt58g07.s
c 125	18	8.0	527	10	BE590865	BE590865	WHE0855.C	c 198	17	7.6	335	9	AA008393	AA008393	ng87b03.r
c 126	18	8.0	533	9	BB703476	BB703476	BB703476	c 199	17	7.6	335	9	AW890166	AW890166	MRO-NF005
c 127	18	8.0	533	10	BF810859	BF810859	RC3-CI016	c 200	17	7.6	336	9	BE172064	BE172064	MRO-NF005
c 128	18	8.0	543	12	AQ523503	AQ523503	HS-5197.A	c 201	17	7.6	337	12	AQ044212	AQ044212	CIT-HSP-2
c 129	18	8.0	579	9	AW820883	AW820883	RC2-ST030	c 202	17	7.6	339	10	W24202	W24202	zb48b12.r1
c 130	18	8.0	588	12	AQ019217	AQ019217	CIT-HSP-2	c 203	17	7.6	345	9	AA452553	AA452553	2x35f08.s
c 131	18	8.0	602	12	AQ925820	AQ925820	RPCI-23-2	c 204	17	7.6	347	9	AA650198	AA650198	ns88a08.s
c 132	18	8.0	605	12	AQ550089	AQ550089	RPCI-11-3	c 205	17	7.6	347	9	AI821817	AI821817	ns88a08.x
c 133	18	8.0	612	9	AV690972	AV690972	AV690972	c 206	17	7.6	347	9	AI821839	AI821839	nt58g07.x
c 134	18	8.0	622	9	AV690973	AV690973	AV690973	c 207	17	7.6	347	10	BM087175	BM087175	499862.MA
c 135	18	8.0	637	10	BG905809	BG905809	TaRr1142F	c 208	17	7.6	353	9	AA536019	AA536019	nt58a05.s
c 136	18	8.0	643	10	BF131759	BF131759	601820350	c 209	17	7.6	355	9	AA371529	AA371529	EST83364
c 137	18	8.0	653	10	BG853624	BG853624	1024037F0	c 210	17	7.6	355	12	A2659693	A2659693	IM0537E17
c 138	18	8.0	665	12	AG050338	AG050338	Pan trogl	c 211	17	7.6	357	10	H67999	H67999	yr76e06.r1
c 139	18	8.0	692	10	BG853623	BG853623	1024037F0	c 212	17	7.6	362	9	AA506053	AA506053	ni03c04.s
c 140	18	8.0	714	10	BG707913	BG707913	602870812	c 213	17	7.6	363	12	AQ683841	AQ683841	HS-5466.A
c 141	18	8.0	729	12	BS22463	BS22463	B0GRM42TR	c 214	17	7.6	365	10	B1042898	B1042898	MR3-OT018
c 142	18	8.0	749	9	AV752575	AV752575	AV752575	c 215	17	7.6	367	10	W71006	W71006	me24h05.r1
c 143	18	8.0	760	10	BG645045	BG645045	EST506664	c 216	17	7.6	368	9	AA834798	AA834798	0498h01.s
c 144	18	8.0	783	10	BM408520	BM408520	EST582847	c 217	17	7.6	369	12	AQ057630	AQ057630	CIT-HSP-2
c 145	18	8.0	803	10	BF692322	BF692322	602249216	c 218	17	7.6	371	12	AQ399104	AQ399104	mgx50019P
c 146	18	8.0	876	10	BE542433	BE542433	601063803	c 219	17	7.6	377	9	AA653760	AA653760	ns89050.s
c 147	18	8.0	933	10	BE729883	BE729883	601564922	c 220	17	7.6	378	9	AI821070	AI821070	ns88a08.y
c 148	18	8.0	937	10	BE895761	BE895761	601432579	c 221	17	7.6	378	9	AW029515	AW029515	wx12a09.x
c 149	18	8.0	1020	10	BM459064	BM459064	AGENCOURT	c 222	17	7.6	378	10	BF229711	BF229711	RC2-CS001
c 150	18	8.0	1067	10	BF125560	BF125560	601763314	c 223	17	7.6	382	9	AI590906	AI590906	tw26g10.x
c 151	18	8.0	1275	10	BG034351	BG034351	602302237	c 224	17	7.6	384	12	BM0183	BM0183	CIT-HSP-204
c 152	18	8.0	1549	10	BF120248	BF120248	601756171	c 225	17	7.6	386	10	BE406858	BE406858	WHE0433.a
c 153	17	7.6	138	9	BE005141	BE005141	MRO-BN011	c 226	17	7.6	388	9	AV612841	AV612841	AV612841
c 154	17	7.6	174	10	BE606387	BE606387	WHE0904.D	c 227	17	7.6	389	10	H19298	H19298	yn50h12.r1
c 155	17	7.6	176	10	W24196	W24196	zb47h12.r1	c 228	17	7.6	390	12	AQ427654	AQ427654	CITFBI-E1-
c 156	17	7.6	213	10	BF1919550	BF1919550	EST539485	c 229	17	7.6	392	12	AZ492787	AZ492787	IM03227F03
c 157	17	7.6	230	10	BF1359954	BF1359954	384734.MA	c 230	17	7.6	393	10	BF229703	BF229703	RC2-CS001
c 158	17	7.6	230	10	BF080979	BF080979	233800.MA	c 231	17	7.6	395	9	AA693662	AA693662	zi50b12.s
c 159	17	7.6	237	12	AQ055357	AQ055357	CIT-HSP-2	c 232	17	7.6	396	9	AA984439	AA984439	am86d08.s
c 160	17	7.6	239	10	BG945117	BG945117	RC6-AN006	c 233	17	7.6	396	12	AQ943234	AQ943234	Sheared.D
c 161	17	7.6	241	10	BF759474	BF759474	RC4-CT065	c 234	17	7.6	401	10	BF229613	BF229613	RC2-CS001
c 162	17	7.6	246	9	AA372881	AA372881	EST84848	c 235	17	7.6	401	12	B41022	B41022	HS-1052-B2-
c 163	17	7.6	252	10	BG999091	BG999091	PM0-HT091								

C 237	17	7.6	10	R19647	R19647 y937e05.r1	C 310	17	7.6	12	AZ728552	AZ728552
C 238	17	7.6	10	BF229671	BF229671 RC2-CS001	C 311	17	7.6	12	AQ373012	AQ373012
C 239	17	7.6	9	A1027309	A1027309 ov93403.x	C 312	17	7.6	12	AQ207175	AQ207175
C 240	17	7.6	409	BF229767	BF229767 RC2-CS001	C 313	17	7.6	554	9	AAW979058
C 241	17	7.6	409	AQ136100	AQ136100 HS_3060_B	C 314	17	7.6	559	9	AAW52738
C 242	17	7.6	412	9	AV614331	C 315	17	7.6	560	10	BF054128
C 243	17	7.6	414	10	BF931135	C 316	17	7.6	561	12	AZ335463
C 244	17	7.6	414	12	AQ881142	C 317	17	7.6	562	12	AQ397263
C 245	17	7.6	415	9	AW857539	C 318	17	7.6	564	12	AQ951938
C 246	17	7.6	415	9	BE005449	C 319	17	7.6	565	10	BE489607
C 247	17	7.6	415	12	AQ884157	C 320	17	7.6	566	10	BE489607
C 248	17	7.6	418	9	A1821706	C 321	17	7.6	566	12	TA174A04Q
C 249	17	7.6	420	12	AQ681765	C 322	17	7.6	568	9	AA127954
C 250	17	7.6	428	9	AA829110	C 323	17	7.6	569	9	AA127954
C 251	17	7.6	434	12	AQ432087	C 324	17	7.6	570	9	AA127954
C 252	17	7.6	437	10	BE343410	C 325	17	7.6	571	9	AA127954
C 253	17	7.6	438	10	BE489637	C 326	17	7.6	575	10	AAW973411
C 254	17	7.6	438	12	AQ696083	C 327	17	7.6	576	9	AAW973411
C 255	17	7.6	440	9	A1298921	C 328	17	7.6	576	9	AAW973411
C 256	17	7.6	440	12	B35169	C 329	17	7.6	578	12	AAW973411
C 257	17	7.6	443	12	AQ437463	C 330	17	7.6	581	9	AAW973411
C 258	17	7.6	444	12	B14192	C 331	17	7.6	582	10	AAW973411
C 259	17	7.6	445	10	H79365	C 332	17	7.6	584	12	AAW973411
C 260	17	7.6	447	12	AQ769119	C 333	17	7.6	584	12	AAW973411
C 261	17	7.6	448	10	BF774976	C 334	17	7.6	587	10	AAW973411
C 262	17	7.6	448	12	B84239	C 335	17	7.6	588	10	AAW973411
C 263	17	7.6	449	12	AQ058688	C 336	17	7.6	590	12	AAW973411
C 264	17	7.6	452	9	BB859448	C 337	17	7.6	593	10	AAW973411
C 265	17	7.6	454	9	AA584195	C 338	17	7.6	594	9	AAW973411
C 266	17	7.6	455	10	BM105131	C 339	17	7.6	595	10	AAW973411
C 267	17	7.6	456	9	A1305255	C 340	17	7.6	597	10	AAW973411
C 268	17	7.6	460	9	AW970913	C 341	17	7.6	599	9	AAW973411
C 269	17	7.6	461	9	AA972523	C 342	17	7.6	604	12	AAW973411
C 270	17	7.6	462	10	BI755750	C 343	17	7.6	610	12	AAW973411
C 271	17	7.6	463	10	BF811705	C 344	17	7.6	611	12	AAW973411
C 272	17	7.6	465	9	A1372312	C 345	17	7.6	611	12	AAW973411
C 273	17	7.6	470	9	A1197544	C 346	17	7.6	612	10	AAW973411
C 274	17	7.6	470	10	RI13744	C 347	17	7.6	616	10	AAW973411
C 275	17	7.6	472	10	BG988781	C 348	17	7.6	631	12	AAW973411
C 276	17	7.6	472	10	BE757995	C 349	17	7.6	636	12	AAW973411
C 277	17	7.6	473	10	BE446150	C 350	17	7.6	638	9	AAW973411
C 278	17	7.6	482	9	AV612705	C 351	17	7.6	646	12	AAW973411
C 279	17	7.6	484	9	AV747231	C 352	17	7.6	646	12	AAW973411
C 280	17	7.6	488	12	AQ174231	C 353	17	7.6	647	9	AAW973411
C 281	17	7.6	488	12	AQ405792	C 354	17	7.6	659	10	AAW973411
C 282	17	7.6	492	9	AW804078	C 355	17	7.6	665	12	AAW973411
C 283	17	7.6	496	9	AI625425	C 356	17	7.6	666	12	AAW973411
C 284	17	7.6	507	10	BF365076	C 357	17	7.6	670	10	AAW973411
C 285	17	7.6	510	10	B825890	C 358	17	7.6	670	10	AAW973411
C 286	17	7.6	515	12	AQ383201	C 359	17	7.6	672	9	AAW973411
C 287	17	7.6	518	10	BI010345	C 360	17	7.6	676	12	AAW973411
C 288	17	7.6	518	12	AZ260693	C 361	17	7.6	681	10	AAW973411
C 289	17	7.6	518	12	AZ260693	C 362	17	7.6	681	10	AAW973411
C 290	17	7.6	519	12	AZ292111	C 363	17	7.6	681	10	AAW973411
C 291	17	7.6	520	10	BF853585	C 364	17	7.6	683	10	AAW973411
C 292	17	7.6	521	10	BI014305	C 365	17	7.6	687	10	AAW973411
C 293	17	7.6	522	12	AQ176563	C 366	17	7.6	687	12	AAW973411
C 294	17	7.6	523	10	BF136759	C 367	17	7.6	688	10	AAW973411
C 295	17	7.6	523	12	AQ669596	C 368	17	7.6	688	10	AAW973411
C 296	17	7.6	526	10	BE517011	C 369	17	7.6	691	12	AAW973411
C 297	17	7.6	527	12	AQ786849	C 370	17	7.6	691	12	AAW973411
C 298	17	7.6	527	12	AQ207481	C 371	17	7.6	707	10	AAW973411
C 299	17	7.6	529	10	BF853586	C 372	17	7.6	707	10	AAW973411
C 300	17	7.6	529	10	BG948063	C 373	17	7.6	711	10	AAW973411
C 301	17	7.6	531	10	BG406916	C 374	17	7.6	717	12	AAW973411
C 302	17	7.6	534	10	BE488266	C 375	17	7.6	718	9	AAW973411
C 303	17	7.6	538	10	BM325351	C 376	17	7.6	718	12	AAW973411
C 304	17	7.6	541	10	BI400855	C 377	17	7.6	725	12	AAW973411
C 305	17	7.6	544	10	BF053868	C 378	17	7.6	728	10	AAW973411
C 306	17	7.6	545	10	BF152190	C 379	17	7.6	735	12	AAW973411
C 307	17	7.6	547	10	T62870	C 380	17	7.6	737	12	AAW973411
C 308	17	7.6	549	9	AI466676	C 381	17	7.6	737	12	AAW973411
C 309	17	7.6	551	10	BE751839	C 382	17	7.6	739	10	AAW973411

c 383	17	7.6	743	10	BJ015349	456	16	7.1	199	9	BB146379	BB146379
c 384	17	7.6	743	12	AG007397	c 457	16	7.1	202	10	W16952	W16952 zb08g03.r1
c 385	17	7.6	744	12	AG173352	c 458	16	7.1	208	12	A2489334	A2489334 1M0321N10
c 386	17	7.6	750	12	BH199724	c 459	16	7.1	211	10	B5672899	B5672899 7d25c03.x
c 387	17	7.6	750	12	AG007400	c 460	16	7.1	217	9	AV239821	AV239821 AV239821
c 388	17	7.6	752	12	AG007399	c 461	16	7.1	219	9	AV901559	AV901559 AV901559
c 389	17	7.6	756	9	AI588143	c 462	16	7.1	216	9	BB302437	BB302437 BB302437
c 390	17	7.6	758	10	BI669270	c 463	16	7.1	226	12	A2921287	A2921287 1006029C0
c 391	17	7.6	761	12	AG032698	c 464	16	7.1	227	9	AI804756	AI804756 tu42409.x
c 392	17	7.6	768	12	A2972942	c 465	16	7.1	227	10	BG017597	BG017597 daa79e06.
c 393	17	7.6	769	10	BE542250	c 466	16	7.1	229	9	AV317439	AV317439 AV317439
c 394	17	7.6	770	10	BG713970	c 467	16	7.1	230	12	AQ481110	AQ481110 RPCI-11-2
c 395	17	7.6	776	12	BH480539	c 468	16	7.1	240	9	AV288565	AV288565 AV288565
c 396	17	7.6	782	10	BG714532	c 469	16	7.1	243	9	BB038794	BB038794 BB038794
c 397	17	7.6	782	10	BI151789	c 470	16	7.1	245	9	AW147880	AW147880 da23a10.x
c 398	17	7.6	791	10	BF214046	c 471	16	7.1	251	10	BI751623	BI751623 Ta01.12f0
c 399	17	7.6	799	12	AZ193878	c 472	16	7.1	252	10	W16815	W16815 zb08c01.r1
c 400	17	7.6	809	9	AL040353	c 473	16	7.1	253	12	AQ507582	AQ507582 RPCI-11-2
c 401	17	7.6	812	12	BH489783	c 474	16	7.1	264	12	BH057512	BH057512 RPCI-24-3
c 402	17	7.6	823	10	BM019985	c 475	16	7.1	265	9	AV258562	AV258562 AV258562
c 403	17	7.6	827	10	BF528552	c 476	16	7.1	266	9	AV175677	AV175677 AV175677
c 404	17	7.6	832	10	BI660501	c 477	16	7.1	266	9	AV327463	AV327463 AV327463
c 405	17	7.6	833	10	BG862446	c 478	16	7.1	267	9	AI967846	AI967846 Ljirnpes
c 406	17	7.6	838	10	BI603609	c 479	16	7.1	269	9	BB072429	BB072429 BB072429
c 407	17	7.6	859	10	BG768315	c 480	16	7.1	273	10	BG013478	BG013478 CM4-GN033
c 408	17	7.6	863	10	BM006752	c 481	16	7.1	275	10	BF458308	BF458308 UI-N-B21-
c 409	17	7.6	867	10	BF538978	c 482	16	7.1	281	9	BI158492	BI158492 BI158492
c 410	17	7.6	870	10	BM006471	c 483	16	7.1	283	10	BI444443	BI444443 dac65f10.
c 411	17	7.6	877	10	BF528686	c 484	16	7.1	284	9	AV064411	AV064411 AV064411
c 412	17	7.6	890	10	BG287064	c 485	16	7.1	284	9	AV219479	AV219479 AV219479
c 413	17	7.6	903	10	BF981937	c 486	16	7.1	285	10	BF871036	BF871036 IL5-ET011
c 414	17	7.6	914	12	CNS041931	c 487	16	7.1	287	9	BB310705	BB310705 BB310705
c 415	17	7.6	915	10	BF530817	c 488	16	7.1	288	9	BB006329	BB006329 BB006329
c 416	17	7.6	929	10	BI453111	c 489	16	7.1	290	9	BB551147	BB551147 BB551147
c 417	17	7.6	931	10	BI198212	c 490	16	7.1	290	12	AQ463174	AQ463174 HS-5199.B
c 418	17	7.6	946	12	CNS03M5G	c 491	16	7.1	293	9	AV312080	AV312080 AV312080
c 419	17	7.6	950	10	BE541026	c 492	16	7.1	295	9	AA018733	AA018733 ze654c02.f
c 420	17	7.6	967	10	BG260685	c 493	16	7.1	295	9	BB134204	BB134204 BB134204
c 421	17	7.6	968	10	BI763476	c 494	16	7.1	296	9	BB290238	BB290238 BB290238
c 422	17	7.6	969	12	CNS03C48	c 495	16	7.1	297	9	BB282453	BB282453 BB282453
c 423	17	7.6	975	9	AL575658	c 496	16	7.1	298	9	AW481529	AW481529 36477.MAR
c 424	17	7.6	978	10	BF791379	c 497	16	7.1	299	9	BB137452	BB137452 BB137452
c 425	17	7.6	983	12	CNS02D51	c 498	16	7.1	301	9	AA350975	AA350975 EST58534
c 426	17	7.6	997	10	BE782589	c 499	16	7.1	301	10	BE825272	BE825272 RC3-CN001
c 427	17	7.6	999	10	BM454451	c 500	16	7.1	302	10	BF944255	BF944255 CM0-NN115
c 428	17	7.6	1001	10	BG546779	c 501	16	7.1	302	12	A2754751	A2754751 cq03e06.f
c 429	17	7.6	1001	12	CNS04OWQ	c 502	16	7.1	304	9	AI646269	AI646269 vv89q02.x
c 430	17	7.6	1002	12	CNS026PE	c 503	16	7.1	304	10	BF456112	BF456112 UI-N-B21-
c 431	17	7.6	1005	10	BG837917	c 504	16	7.1	305	9	BB393769	BB393769 BB393769
c 432	17	7.6	1012	10	BF676440	c 505	16	7.1	310	10	BI129749	BI129749 G094P95Y
c 433	17	7.6	1027	9	BB611485	c 506	16	7.1	310	10	BM153396	BM153396 TCBAp2D11
c 434	17	7.6	1027	9	BB611485	c 507	16	7.1	311	9	BB406144	BB406144 BB406144
c 435	17	7.6	1040	10	BM457219	c 508	16	7.1	312	9	BB400774	BB400774 BB400774
c 436	17	7.6	1073	10	BF161584	c 509	16	7.1	314	12	BH352671	BH352671 CH230-81K
c 437	17	7.6	1113	12	CNS01TW6	c 510	16	7.1	315	9	AI415086	AI415086 mu95608.x
c 438	17	7.6	1139	10	BF166113	c 511	16	7.1	316	9	AI666579	AI666579 mu19004.x
c 439	17	7.6	1193	12	AG069635	c 512	16	7.1	317	10	BG413835	BG413835 de73e07.x
c 440	17	7.6	1205	10	BF159163	c 513	16	7.1	318	10	BM276962	BM276962 952013E09
c 441	17	7.6	1375	10	BG682873	c 514	16	7.1	319	9	AW673093	AW673093 ba57b11.y
c 442	17	7.6	1377	10	BF900120	c 515	16	7.1	321	10	BG022754	BG022754 daa79g08.
c 443	16	7.1	81	12	A2946005	c 516	16	7.1	322	9	BB458677	BB458677 BB458677
c 444	16	7.1	104	10	Z32869	c 517	16	7.1	322	9	BB507332	BB507332 BB507332
c 445	16	7.1	114	10	BG001900	c 518	16	7.1	322	10	BG017610	BG017610 daa79g08.
c 446	16	7.1	139	10	BF995170	c 519	16	7.1	323	12	AZ715881	AZ715881 RPCI-24-8
c 447	16	7.1	156	10	U44250	c 520	16	7.1	328	10	BG348058	BG348058 de73e07.y
c 448	16	7.1	169	9	BB563163	c 521	16	7.1	329	9	BB207721	BB207721 BB207721
c 449	16	7.1	179	10	BF948588	c 522	16	7.1	329	9	BB586422	BB586422 BB586422
c 450	16	7.1	183	10	Z20297	c 523	16	7.1	332	9	AI783676	AI783676 tu28509.x
c 451	16	7.1	187	10	BF951111	c 524	16	7.1	332	9	BB207720	BB207720 BB207720
c 452	16	7.1	191	9	AV232272	c 525	16	7.1	339	9	AA642536	AA642536 nq72606.s
c 453	16	7.1	191	10	F18390	c 526	16	7.1	343	9	BB313131	BB313131 BB313131
c 454	16	7.1	195	9	BB009108	c 527	16	7.1	344	9	AA158837	AA158837 zo58f04.f
c 455	16	7.1	195	10	F31449	c 528	16	7.1	344	9	BB548994	BB548994 BB548994

c 529	16	7.1	344	10	BF851763	BE851763 CM3-EN007	c 602	16	7.1	417	12	AQ566137	AQ566137 HS-5374-A
c 530	16	7.1	346	9	AA729166	AA729166 nx54f07.s	603	16	7.1	418	9	AV907156	AV907156 AV907156
c 531	16	7.1	349	10	BI18602	BI18602 1031029B0	604	16	7.1	420	9	AV839516	AV839516 AV839516
c 532	16	7.1	351	9	AW822455	AW822455 uq21b09.x	605	16	7.1	420	9	AV897126	AV897126 AV897126
c 533	16	7.1	351	10	BG410841	BG410841 EM1_26.F0	c 606	16	7.1	420	10	BG518004	BG518004 947065F08
c 534	16	7.1	351	10	BG979583	BG979583 CM4-CND06	607	16	7.1	421	9	AV902662	AV902662 AV902662
c 535	16	7.1	352	12	AQ706609	AQ706609 HS-5533-B	608	16	7.1	421	9	AV904429	AV904429 AV904429
c 536	16	7.1	353	10	BE933270	BE933270 UI-M-BZ1-B	609	16	7.1	421	9	BE096660	BE096660 UI-R-BU0-
c 537	16	7.1	356	9	AV892535	AV892535 AV892535	c 610	16	7.1	421	12	AQ0902360	AQ0902360 LMAJFV1_1
c 538	16	7.1	356	9	AW905140	AW905140 QV0-NN107	611	16	7.1	422	10	BF176719	BF176719 NCST3a16
c 539	16	7.1	357	12	BH457195	BH457195 BOHGG67TR	612	16	7.1	422	10	BF176719	BF176719 NCST3a16
c 540	16	7.1	362	12	AQ309589	AQ309589 CITBI-E1-	c 613	16	7.1	424	9	AA406547	AA406547 2v12h03.s
c 541	16	7.1	363	12	AZ586192	AZ586192 1M0391K22	c 614	16	7.1	424	9	AA406547	AA406547 2v12h03.s
c 542	16	7.1	363	12	AZ586192	AZ586192 1M0391K22	c 615	16	7.1	424	9	AA406547	AA406547 2v12h03.s
c 543	16	7.1	369	10	BF843983	BF843983 MR2-HT104	c 616	16	7.1	424	9	AA406547	AA406547 2v12h03.s
c 544	16	7.1	371	9	AA865337	AA865337 AV865337	c 617	16	7.1	429	10	BI993068	BI993068 1020072D0
c 545	16	7.1	372	9	AA427065	AA427065 ve78e03.r	618	16	7.1	429	10	BI993068	BI993068 1020072D0
c 546	16	7.1	374	9	BB696317	BB696317 BB696317	c 619	16	7.1	430	9	AI035819	AI035819 uc88f10.y
c 547	16	7.1	374	10	Z46137	Z46137 HSC18C051.n	c 620	16	7.1	430	9	AV896789	AV896789 AV896789
c 548	16	7.1	374	12	AQ310833	AQ310833 CITBI-E1-	c 621	16	7.1	433	10	BF820463	BF820463 MRI-RT003
c 549	16	7.1	376	9	AI059219	AI059219 UI-R-C1-1	c 622	16	7.1	433	10	BF820463	BF820463 MRI-RT003
c 550	16	7.1	377	9	AV837129	AV837129 AV837129	c 623	16	7.1	436	10	BG407706	BG407706 dd20h11.x
c 551	16	7.1	377	9	AA325462	AA325462 EST28450	c 624	16	7.1	436	12	CNS07H99	CNS07H99 ANopheles
c 552	16	7.1	379	9	AA984232	AA984232 am82g06.s	c 625	16	7.1	436	9	AA874539	AA874539 vx03e07.r
c 553	16	7.1	379	9	AV853189	AV853189 AV853189	c 626	16	7.1	438	10	R17577	R17577 y914a11.r1
c 554	16	7.1	383	9	AA067067	AA067067 mm31e09.r	c 627	16	7.1	439	9	AW338783	AW338783 ha65h10.x
c 555	16	7.1	386	9	AV870675	AV870675 AV870675	c 628	16	7.1	439	12	AZ459188	AZ459188 LM0263P14
c 556	16	7.1	388	10	R64467	R64467 y116a08.r1	c 629	16	7.1	441	10	BF893533	BF893533 QV1-MT013
c 557	16	7.1	388	12	AQ495493	AQ495493 HS-5211-B	c 630	16	7.1	441	10	BF893533	BF893533 QV1-MT013
c 558	16	7.1	391	9	AV897147	AV897147 AV897147	c 631	16	7.1	443	9	BE076334	BE076334 CM1-BT059
c 559	16	7.1	392	9	AV895773	AV895773 AV895773	c 632	16	7.1	444	9	AU066285	AU066285 AU066285
c 560	16	7.1	397	9	AW82231	AW82231 41456 MAR	c 633	16	7.1	444	12	AQ558865	AQ558865 HS-2089-B
c 561	16	7.1	397	10	BE944046	BE944046 UI-M-BH3-	c 634	16	7.1	445	9	AA266107	AA266107 mz51g06.r
c 562	16	7.1	398	9	AV864004	AV864004 AV864004	c 635	16	7.1	445	10	BF655307	BF655307 279765 MA
c 563	16	7.1	398	10	BF892132	BF892132 QV1-MT013	c 636	16	7.1	446	9	AA729805	AA729805 nx39e06.s
c 564	16	7.1	399	9	AA171478	AA171478 2p22d01.s	c 637	16	7.1	446	9	AW861209	AW861209 RC1-CT030
c 565	16	7.1	400	9	AA415672	AA415672 50102 MAR	c 638	16	7.1	446	10	BE718971	BE718971 RC3-HT083
c 566	16	7.1	401	9	AV860844	AV860844 AV860844	c 639	16	7.1	447	10	R19678	R19678 y935a07.r1
c 567	16	7.1	401	9	AV896083	AV896083 AV896083	c 640	16	7.1	450	9	BF790457	BF790457 BF790457
c 568	16	7.1	401	10	BI446945	BI446945 daa90h08.	c 641	16	7.1	450	12	AG186763	AG186763 Homo sap1
c 569	16	7.1	403	9	AV865321	AV865321 AV865321	c 642	16	7.1	453	9	AI926981	AI926981 wo68e01.x
c 570	16	7.1	403	9	AW804596	AW804596 QV0-UM009	c 643	16	7.1	453	9	AA608979	AA608979 af05c12.s
c 571	16	7.1	403	10	R38317	R38317 yH95403.s1	c 644	16	7.1	454	10	BI135132	BI135132 UI-M-BH3-
c 572	16	7.1	403	10	W44038	W44038 mc74g01.r1	c 645	16	7.1	454	10	BF600634	BF600634 265376 MA
c 573	16	7.1	404	10	R09912	R09912 yf30a08.r1	c 646	16	7.1	457	10	BF600634	BF600634 265376 MA
c 574	16	7.1	406	9	AV848545	AV848545 AV848545	c 647	16	7.1	458	10	BG518003	BG518003 947065F08
c 575	16	7.1	407	9	AV841975	AV841975 AV841975	c 648	16	7.1	458	12	AQ699246	AQ699246 HS-5569-A
c 576	16	7.1	407	9	AV862244	AV862244 AV862244	c 649	16	7.1	459	12	AQ017378	AQ017378 CIT-HSP-2
c 577	16	7.1	407	9	AV901174	AV901174 AV901174	c 650	16	7.1	459	12	AZ712050	AZ712050 RPTI-24-1
c 578	16	7.1	407	9	AV901325	AV901325 AV901325	c 651	16	7.1	460	12	FR0022708	FR0022708 F rubripe
c 579	16	7.1	408	9	AV852597	AV852597 AV852597	c 652	16	7.1	461	10	BE817010	BE817010 RC0-BN024
c 580	16	7.1	408	9	BE192164	BE192164 db88c06.x	c 653	16	7.1	462	9	BB761315	BB761315 BB761315
c 581	16	7.1	409	9	AV899912	AV899912 AV899912	c 654	16	7.1	463	9	AV598759	AV598759 AV598759
c 582	16	7.1	409	10	BM498701	BM498701 952020A08	c 655	16	7.1	463	12	AQ041356	AQ041356 CIT-HSP-2
c 583	16	7.1	409	12	AZ076309	AZ076309 NCW01E12T	c 656	16	7.1	463	12	AQ309445	AQ309445 CITBI-E1-
c 584	16	7.1	410	9	AI399073	AI399073 NCW01E12T	c 657	16	7.1	464	12	CNS07GAO	CNS07GAO ANopheles
c 585	16	7.1	410	9	AV861929	AV861929 AV861929	c 658	16	7.1	464	12	BF944704	BF944704 QV0-NN114
c 586	16	7.1	410	12	AQ205980	AQ205980 HS-3236-B	c 659	16	7.1	465	12	AQ295107	AQ295107 HS-3004-A
c 587	16	7.1	411	10	BM498728	BM498728 952020E07	c 660	16	7.1	466	10	T21833	T21833 3841 Lambda
c 588	16	7.1	412	9	AV846051	AV846051 AV846051	c 661	16	7.1	471	10	BF252598	BF252598 EST419860
c 589	16	7.1	413	9	AV896577	AV896577 AV896577	c 662	16	7.1	471	12	AQ783699	AQ783699 HS-3098-B
c 590	16	7.1	414	9	AI928087	AI928087 wo66h12.x	c 663	16	7.1	472	10	BF441823	BF441823 258248 MA
c 591	16	7.1	414	10	BF999714	BF999714 RC2-GN013	c 664	16	7.1	472	10	BF441823	BF441823 258248 MA
c 592	16	7.1	414	10	BI012881	BI012881 PM4-ET067	c 665	16	7.1	473	10	BM079008	BM079008 MES788-A1
c 593	16	7.1	415	9	AA026783	AA026783 ze93d11.r	c 666	16	7.1	473	10	BM289388	BM289388 530995 MA
c 594	16	7.1	415	9	AA452567	AA452567 zx35h01.s	c 667	16	7.1	474	9	AI769883	AI769883 w130a01.x
c 595	16	7.1	416	9	AF077296	AF077296 AF077296	c 668	16	7.1	474	9	W87326	W87326 zh64e08.r1
c 596	16	7.1	416	9	AA446066	AA446066 FLC6468.H	c 669	16	7.1	474	10	BF440667	BF440667 256641 MA
c 597	16	7.1	416	9	AV900126	AV900126 AV900126	c 670	16	7.1	477	9	AI552874	AI552874 mm31e09.y
c 598	16	7.1	416	9	AV906603	AV906603 AV906603	c 671	16	7.1	478	9	AW633008	AW633008 bl02a08.x
c 599	16	7.1	417	9	AI964974	AI964974 fc85a11.y	c 672	16	7.1	480	9	AW980958	AW980958 EST32119
c 600	16	7.1	417	9	AV893540	AV893540 AV893540	c 673	16	7.1	480	9	BE156531	BE156531 QV0-HT036
c 601	16	7.1	417	9	AV906597	AV906597 AV906597	c 674	16	7.1	480	10	BF441819	BF441819 258242 MA

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c 676	16	7.1	484	12	BJ093132	BJ093132	749	16	7.1	562	10	BI774808	BI774808 467029 MA
c 677	16	7.1	485	10	BH108858	RPCI-24-2	c 750	16	7.1	563	9	AI517070	AI517070 GH2702.5
c 678	16	7.1	487	10	BI580449	RE74645.5	c 751	16	7.1	563	10	BJ049561	BJ049561 BJ049561
c 679	16	7.1	488	12	FR0048003	AI444788 Fugu rubr	c 752	16	7.1	565	9	AI344329	AI344329 tc03f09.x
c 680	16	7.1	489	10	BI159398	BG159398 OV2_7_D02	c 753	16	7.1	566	10	BG537090	BG537090 602565176
c 681	16	7.1	490	12	AQ114864	AQ114864 CIT-HSP-2	c 754	16	7.1	566	10	BM072796	BM072796 MEST53-GO
c 682	16	7.1	491	12	BH1894	BI1894 RPCI111-11K7	c 755	16	7.1	566	10	BM261639	BM261639 da147d02.
c 683	16	7.1	492	10	BG382525	BG382525 298451 MA	c 756	16	7.1	567	9	AV916550	AV916550 AV516550
c 684	16	7.1	493	12	AQ477994	AQ477994 CITBI-EI-	c 757	16	7.1	568	9	AW752914	AW752914 MR2-CT022
c 685	16	7.1	494	12	BG023546	BG023546 dab62d06.	c 758	16	7.1	569	12	AZ613136	AZ613136 1M0441B23
c 686	16	7.1	495	10	AQ136929	AQ136929 HS_2221.A	c 759	16	7.1	570	12	AZ079886	AZ079886 RPCI-23-4
c 687	16	7.1	496	10	BF615094	BF615094 GDB1D08.x	c 760	16	7.1	571	9	AA894611	AA894611 oJ57903.s
c 688	16	7.1	497	9	AA745480	AA745480 ny64408.s	c 761	16	7.1	575	10	BM272141	BM272141 1g39f01.x
c 689	16	7.1	498	10	H29611	H29611 ym61e04.s1	c 762	16	7.1	580	12	AZ828075	AZ828075 2M0104D21
c 690	16	7.1	499	12	AA452979	AA452979 z4x1804.r	c 763	16	7.1	580	12	BH108255	BH108255 RPCI-24-3
c 691	16	7.1	500	10	BG668168	BG668168 156722 MA	c 764	16	7.1	581	12	AO614839	AO614839 HS_5140.A
c 692	16	7.1	501	10	AQ316415	AQ316415 RPCI111-10	c 765	16	7.1	582	12	BH078788	BH078788 RPCI-24-2
c 693	16	7.1	502	10	AI853716	AI853716 UI-M-BHO-	c 766	16	7.1	583	9	AW499780	AW499780 UI-HF-BP0
c 694	16	7.1	503	9	AI315098	AI315098 dah39g11.	c 767	16	7.1	583	10	BJ010100	BJ010100 BJ010100
c 695	16	7.1	504	10	BI384675	BI384675 fb12g12.y	c 768	16	7.1	583	10	BF091005	BF091005 BJ091005
c 696	16	7.1	505	10	BF817924	BF817924 MR2-CI012	c 769	16	7.1	584	9	AI664897	AI664897 605004A09
c 697	16	7.1	506	10	BG698596	BG698596 RCI-UT003	c 770	16	7.1	586	12	AQ484295	AQ484295 RPCI-11-2
c 698	16	7.1	507	9	AA364499	AA364499 LD08271.5	c 771	16	7.1	587	9	AL654533	AL654533 AL654533
c 699	16	7.1	508	10	BF770560	BF770560 RCI-IT001	c 772	16	7.1	588	9	AW587301	AW587301 EST318924
c 700	16	7.1	509	10	BM347223	BM347223 C3-11F2 H	c 773	16	7.1	591	10	BI995621	BI995621 103102980
c 701	16	7.1	510	12	AQ247750	AQ247750 HS_2063.A	c 774	16	7.1	592	10	BJ100402	BJ100402 F.rubripe
c 702	16	7.1	511	10	AA986501	AA986501 ue14a09.x	c 775	16	7.1	596	12	FR0027156	FR0027156
c 703	16	7.1	512	9	AA386501	AA386501 ue14a09.x	c 776	16	7.1	598	10	BE430602	BE430602 SUN004.G0
c 704	16	7.1	513	10	BJ053564	BJ053564 BJ053564	c 777	16	7.1	599	9	AV545951	AV545951 AV545951
c 705	16	7.1	514	10	BE490666	BE490666 WHE0369.H	c 778	16	7.1	602	12	BH484174	BH484174 BOHRC63TF
c 706	16	7.1	515	9	AV754450	AV754450 AV754450	c 779	16	7.1	603	9	AW636521	AW636521 b147f10.w
c 707	16	7.1	516	10	BI946387	BI946387 01130 lea	c 780	16	7.1	605	9	AI727008	AI727008 BNLGH710
c 708	16	7.1	517	10	AW767080	AW767080 dab2g04.y	c 781	16	7.1	605	12	AZ899803	AZ899803 RPCI-24-2
c 709	16	7.1	518	10	BG020458	BG020458 dc78a09.x	c 782	16	7.1	606	10	BM226376	BM226376 K0227B11-
c 710	16	7.1	519	12	BF343029	BF343029 602017141	c 783	16	7.1	608	10	BI352806	BI352806 GM20880.5
c 711	16	7.1	520	12	AZ629190	AZ629190 LM0482E06	c 784	16	7.1	610	9	AV661980	AV661980 AV661980
c 712	16	7.1	521	9	AA759397	AA759397 vw64b05.r	c 785	16	7.1	611	12	AZ837322	AZ837322 2M0132105
c 713	16	7.1	522	9	AA172863	AA172863 ms20a03.r	c 786	16	7.1	612	9	AL650875	AL650875 AL650875
c 714	16	7.1	523	10	BF078055	BF078055 228299 MA	c 787	16	7.1	614	12	AZ257126	AZ257126 RPCI-23-1
c 715	16	7.1	524	10	BG554517	BG554517 de93c12.x	c 788	16	7.1	615	12	AZ376909	AZ376909 LM0131D11
c 716	16	7.1	525	10	BI706767	BI706767 fq09b03.y	c 789	16	7.1	617	9	AI999129	AI999129 701554551
c 717	16	7.1	526	9	AW047994	AW047994 UI-M-BHI-	c 790	16	7.1	617	10	BI045860	BI045860 MR3-FN020
c 718	16	7.1	527	9	BB759332	BB759332 BB759332	c 791	16	7.1	618	12	FR0004858	FR0004858 F.rubripes
c 719	16	7.1	528	10	BF853820	BF853820 MR2-EN009	c 792	16	7.1	619	12	FR0029796	FR0029796 Fugu rubr
c 720	16	7.1	529	10	AA282639	AA282639 zs90d08.r	c 793	16	7.1	621	10	BF814762	BF814762 MR2-CI012
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c 730	16	7.1	539	12	AQ936792	AQ936792 JNB-327C	c 803	16	7.1	630	10	BJ032737	BJ032737 BJ032737
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c 732	16	7.1	541	9	AV663992	AV663992 AV663992	c 805	16	7.1	633	10	BE374471	BE374471 601227447
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c 738	16	7.1	547	10	BJ050262	BJ050262 BJ050262	c 811	16	7.1	637	10	BJ060101	BJ060101 BJ060101
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## ALIGNMENTS

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ORGANISM Homo sapiens
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Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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## FEATURES

source

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insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L10M11010 row: k column: 24  
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Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.5 kb. Library prepared by Life  
Technologies."

BASE COUNT 170 a 227 c 212 g 158 t 1 others  
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Query Match          69.8%; Score 157; DB 10; Length 768;
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|||||

QY 64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGGCCACCTGCGTGGCCCTCTCC 123
|||||
Db 601 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGGCCACCTGCGTGGCCCTCTCC 660
|||||

QY 124 TACGATGGCCTGCTGGTGACAAATCAGATCATGCCCA 160
|||||
Db 661 TACGATGGCCTGCTGGTGACAAATCAGATCATGCCCA 697
|||||

RESULT 3
BG476912          BG476912          776 bp mRNA linear EST 21-MAR-2001
LOCUS
DEFINITION 602524881F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4642868 5',
mRNA sequence.
ACCESSION BG476912
VERSION BG476912
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 776)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1412 row: b column: 21
High quality sequence stop: 747.
FEATURES
source
1..776
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4642868"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

BASE COUNT 180 a 197 c 232 g 167 t

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Query Match          69.8%; Score 157; DB 10; Length 776;
Best Local Similarity 100.0%; Pred. No. 5.6e-70;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCTTCAGCTGGTCTTTGGCATCGAG 63
|||||
Db 194 TTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCTTCAGCTGGTCTTTGGCATCGAG 253
|||||

QY 64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGGCCACCTGCGTGGCCCTCTCC 123
|||||
```

```
Db 254 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGGCCACCTGCGTGGCCCTCTCC 313
|||||
QY 124 TACGATGGCCTGCTGGTGACAAATCAGATCATGCCCA 160
|||||
Db 314 TACGATGGCCTGCTGGTGACAAATCAGATCATGCCCA 350
|||||

RESULT 4
BG397171          BG397171          878 bp mRNA linear EST 12-MAR-2001
LOCUS
DEFINITION 602434130F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4552086 5',
mRNA sequence.
ACCESSION BG397171
VERSION BG397171
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 878)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1247 row: l column: 07
High quality sequence stop: 866.
FEATURES
source
1..878
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4552086"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

BASE COUNT 197 a 214 c 262 g 205 t

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Query Match          69.8%; Score 157; DB 10; Length 878;
Best Local Similarity 100.0%; Pred. No. 5.8e-70;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCTTCAGCTGGTCTTTGGCATCGAG 63
|||||
Db 193 TTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCTTCAGCTGGTCTTTGGCATCGAG 252
|||||

QY 64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGGCCACCTGCGTGGCCCTCTCC 123
|||||
Db 253 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGGCCACCTGCGTGGCCCTCTCC 312
|||||

QY 124 TACGATGGCCTGCTGGTGACAAATCAGATCATGCCCA 160
|||||
Db 313 TACGATGGCCTGCTGGTGACAAATCAGATCATGCCCA 349
|||||

RESULT 5
```

BG476078	602520963F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4639670 5', mRNA sequence.
LOCUS	886 bp mRNA linear EST 21-MAR-2001
DEFINITION	
ACCESSION	BG476078
VERSION	BG476078.1 GI:13408357
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 886)
TITLE	NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/DMP cDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LICM1403 row: m column: 15 High quality sequence stop: 730.
FEATURES	Location/Qualifiers
source	1..886 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4639670" /clone_lib="NIH_MGC_20" /tissue_type="melanotic melanoma" /lab_host="DH10B (phage-resistant)" /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life technologies)."
BASE COUNT	183 a 231 c 262 g 210 t
ORIGIN	
Query Match	69.8%; Score 157; DB 10; Length 886;
Best Local Similarity	100.0%; Pred. No. 5.8e-70;
Matches 157; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY 4	TTCTTTCTGTGATCTCAGCAAGCTTCGGATTCTTGCGAGTGGTCTTTGGCATCGAG 63
Db	97 TTCTTTCTGTGATCTTTCAGAAAGCTTCGGATCTCTTGCGAGTGGTCTTTGGCATCGAG 156
QY 64	CTCATGAAGTGCACCCATCGGCCACGTGTACATCTTCCACCTGCCTGGCCCTCTCC 123
Db	157 CTGATGAAGTGCACCCATCGGCCACGTGTACATCTTGGCCACCTGCCTGGCCCTCTCC 216
QY 124	TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCA 160
Db	217 TAGCATGGCCTGCTGGGTGACAATCAGATCATGCCCA 253
RESULT 6	
BG765817	602739647F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4865682 5', mRNA sequence.
LOCUS	894 bp mRNA linear EST 15-MAY-2001
DEFINITION	
ACCESSION	BG765817
VERSION	BG765817.1 GI:14076470
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

Tissue Procurement: ATCC/DCTD/DTP  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LCM1672 row: k column: 01  
 High quality sequence stop: 619.  
 Location/Qualifiers  
 1..707  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4840824"  
 /clone\_lib="NIH\_MGC\_49"  
 /tissue\_type="melanotic melanoma, high MDR (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site:2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
 into EcoRI/XhoI sites using the following 5' adaptor:  
 GGCACGAG(G). Size-selected >500bp for average insert size  
 1.8kb. Library constructed by Ling Hong in the laboratory  
 of Gerald M. Rubin (University of California, Berkeley)  
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
 II RT (Life Technologies). Note: this is a NIH\_MGC  
 Library."
   
 BASE COUNT 145 a 241 c 186 g 135 t  
 ORIGIN

## FEATURES

source

Query Match 60.9%; Score 137; DB 10; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 1e-59;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 TTCTTTCTGTGATCTTCCGAAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63  
 Db 402 TTCTTTCTGTGATCTTCCGAAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 461  
 QY 64 CTGATGGAGTGGACCCATCGGCACGCTGATCTTTGGCCACCTGCGTGGCCCTCTCC 123  
 Db 462 CTGATGGAGTGGACCCATCGGCACGCTGATCTTTGGCCACCTGCGTGGCCCTCTCC 521  
 QY 124 TACGATGGCCTGCTGGG 140  
 Db 522 TACGATGGCCTGCTGGG 538

Query Match 60.9%; Score 137; DB 10; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 1e-59;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCCGAAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63  
 Db 402 TTCTTTCTGTGATCTTCCGAAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 461  
 QY 64 CTGATGGAGTGGACCCATCGGCACGCTGATCTTTGGCCACCTGCGTGGCCCTCTCC 123  
 Db 462 CTGATGGAGTGGACCCATCGGCACGCTGATCTTTGGCCACCTGCGTGGCCCTCTCC 521  
 QY 124 TACGATGGCCTGCTGGG 140  
 Db 522 TACGATGGCCTGCTGGG 538

RESULT 8  
 BF792356  
 LOCUS  
 DEFINITION 602252896F1 NIH\_MGC\_84 Homo sapiens cDNA clone IMAGE:4345222 5',  
 mRNA sequence.  
 ACCESSION BF792356  
 VERSION BF792356.1 GI:12097410  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 876)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM9964 row: p column: 23

QY 4 TTCTTTCTGTGATCTTCCGAAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63  
 Db 402 TTCTTTCTGTGATCTTCCGAAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 461  
 QY 64 CTGATGGAGTGGACCCATCGGCACGCTGATCTTTGGCCACCTGCGTGGCCCTCTCC 123  
 Db 462 CTGATGGAGTGGACCCATCGGCACGCTGATCTTTGGCCACCTGCGTGGCCCTCTCC 521  
 QY 124 TACGATGGCCTGCTGGG 140  
 Db 522 TACGATGGCCTGCTGGG 538

FEATURES High quality sequence stop: 780.  
 Location/Qualifiers  
 1..876  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4345222"  
 /clone\_lib="NIH\_MGC\_84"  
 /tissue\_type="adrenal cortex carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site:1:  
 NotI; Site:2: SalI; Cloned unidirectionally; oligo-dT  
 primed. Average insert size 1.229 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC library."
   
 BASE COUNT 185 a 215 c 248 g 228 t  
 ORIGIN

Query Match 60.9%; Score 137; DB 10; Length 876;  
 Best Local Similarity 100.0%; Pred. No. 1e-59;  
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 24 CAAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATCGAGTGAAGTGGACCCCAT 83  
 Db 101 CAAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATCGAGTGAAGTGGACCCCAT 160  
 QY 84 CGGCCACGTGTACATCTTTGGCCACCTGCGTGGCCCTCTCTACGATGGCCTGCTGGGTGA 143  
 Db 161 CGGCCACGTGTACATCTTTGGCCACCTGCGTGGCCCTCTCTACGATGGCCTGCTGGGTGA 220  
 QY 144 CAATCAGATCATGCCCA 160  
 Db 221 CAATCAGATCATGCCCA 237

RESULT 9  
 BM470991  
 LOCUS  
 DEFINITION AGENCOURT\_6478212 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:5562971  
 5', mRNA sequence.  
 ACCESSION BM470991  
 VERSION BM470991.1 GI:18520033  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1021)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: ATCC/DCTD/DTP  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM12293 row: d column: 12  
 High quality sequence stop: 725.  
 Location/Qualifiers  
 1..1021

FEATURES source  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5562971"  
 /clone\_lib="NIH\_MGC\_72"  
 /tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI;  
 Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 2 kb. Library constructed by Life

BASE COUNT 232 a 290 c 292 g 206 t 1 others  
ORIGIN

Query Match 56.9%; Score 128; DB 10; Length 1021;  
Best Local Similarity 100.0%; Pred. No. 4.7e-55;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGTCTTTGGCATCGAG 63  
|||||  
Db 596 TTCTTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGTCTTTGGCATCGAG 655  
|||||

QY 64 CTGATGAAGTGGACCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 123  
|||||

Db 656 CTGATGAAGTGGACCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 715  
|||||

QY 124 TACCATGG 131  
Db 716 TACCATGG 723

RESULT 10  
BE541476  
LOCUS BE541476 795 bp mRNA linear EST 09-AUG-2000  
DEFINITION 601067928F1 NIH\_MGC\_10 Homo sapiens cDNA clone IMAGE:3454135 5',  
mRNA sequence.  
ACCESSION BE541476  
VERSION BE541476.1 GI:9770121  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 795)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM8438 row: h column: 08  
High quality sequence stop: 662.  
Location/Qualifiers  
1..795  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3454135"  
/clone\_lib="NIH\_MGC\_10"  
/cell\_line="MGC36"  
/lab\_host="DH10B"  
/note="organ: cervix; Vector: pCMV-Sport6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.5 Kb. Library prepared by Life  
Technologies."

BASE COUNT 182 a 199 c 234 g 180 t  
ORIGIN

Query Match 48.0%; Score 108; DB 10; Length 795;  
Best Local Similarity 100.0%; Pred. No. 8.5e-45;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 TTGGATCGAGCTGATGGAAGTGGACCCATCGGCCACGTGTACATCTTTGCCACTGCC 112  
|||||

Db 238 TTGGATCGAGCTGATGGAAGTGGACCCATCGGCCACGTGTACATCTTTGCCACTGCC 297  
|||||

BASE COUNT 182 a 199 c 234 g 180 t  
ORIGIN

Query Match 48.0%; Score 108; DB 10; Length 795;  
Best Local Similarity 100.0%; Pred. No. 8.5e-45;  
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 TTGGATCGAGCTGATGGAAGTGGACCCATCGGCCACGTGTACATCTTTGCCACTGCC 112  
|||||

Db 238 TTGGATCGAGCTGATGGAAGTGGACCCATCGGCCACGTGTACATCTTTGCCACTGCC 297  
|||||

QY 113 TGGCCCTCTCTACGATGGCCTGCTGGTGACAATCAGATCATGCCCA 160  
|||||

Db 298 TGGCCCTCTCTACGATGGCCTGCTGGTGACAATCAGATCATGCCCA 345  
|||||

RESULT 11  
BE733003  
LOCUS BE733003 696 bp mRNA linear EST 15-SEP-2000  
DEFINITION 601569780F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:3844482 5',  
mRNA sequence.  
ACCESSION BE733003  
VERSION BE733003.1 GI:10146995  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 696)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: L1CM540 row: p column: 19  
High quality sequence stop: 693.  
Location/Qualifiers  
1..696  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3844482"  
/clone\_lib="NIH\_MGC\_21"  
/tissue\_type="choriocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: placenta; Vector: pORF7; Site\_1: XhoI;  
Site\_2: EcoRI; CDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 142 a 206 c 204 g 144 t  
ORIGIN

Query Match 46.2%; Score 104; DB 10; Length 696;  
Best Local Similarity 100.0%; Pred. No. 9.4e-43;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGTCTTTGGCATCGAG 63  
|||||

Db 560 TTCTTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGTCTTTGGCATCGAG 619  
|||||

QY 64 CTGATGAAGTGGACCCATCGGCCACGTGTACATCTTTGCCAC 107  
|||||

Db 620 CTGATGAAGTGGACCCATCGGCCACGTGTACATCTTTGCCAC 663  
|||||

BASE COUNT 142 a 206 c 204 g 144 t  
ORIGIN

Query Match 46.2%; Score 104; DB 10; Length 696;  
Best Local Similarity 100.0%; Pred. No. 9.4e-43;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGTCTTTGGCATCGAG 63  
|||||

Db 560 TTCTTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGTCTTTGGCATCGAG 619  
|||||

QY 64 CTGATGAAGTGGACCCATCGGCCACGTGTACATCTTTGCCAC 107  
|||||

Db 620 CTGATGAAGTGGACCCATCGGCCACGTGTACATCTTTGCCAC 663  
|||||

RESULT 12  
BG764972  
LOCUS BG764972 704 bp mRNA linear EST 15-MAY-2001  
DEFINITION 602737745F1 NIH\_MGC\_49 Homo sapiens cDNA clone IMAGE:4863059 5',  
mRNA sequence.  
ACCESSION BG764972  
VERSION BG764972.1 GI:14075625  
KEYWORDS EST.  
SOURCE human.

DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
 Plate: LLCM541 row: j column: 04  
 High quality sequence stop: 742.

FEATURES  
 source  
 Location/Qualifiers  
 1. .760  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3844707"  
 /clone\_lib="NIH\_MGC\_21"  
 /tissue\_type="choriocarcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: placenta; Vector: pOTB7; Site\_1: XhoI;  
 Site\_2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."  
 166 a 220 c 216 g 158 t

BASE COUNT  
 ORIGIN

Query Match 44.9%; Score 101; DB 10; Length 760;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-41;  
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCCCTGTATCTTCACGAAGCTTCGGATCCCTTGGACGTGGCTTTGGCATCGAG 63  
 Db 545 TTCTTTCCCTGTATCTTCACGAAGCTTCGGATCCCTTGGACGTGGCTTTGGCATCGAG 604

QY 64 CTGATGGAAGTGGACCCATCGGCCACGTGTACATCTTTGC 104  
 Db 605 CTGATGGAAGTGGACCCATCGGCCACGTGTACATCTTTGC 645

RESULT 14  
 BE734462 1101 bp mRNA linear EST 15-SEP-2000  
 LOCUS 601566241F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:3841042 5',  
 DEFINITION mRNA sequence.  
 BE734462  
 BE734462.1 GI:10148454  
 EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
 Plate: LLCM532 row: a column: 11  
 High quality sequence stop: 709.

FEATURES  
 source  
 Location/Qualifiers  
 1. .1101  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3841042"  
 /clone\_lib="NIH\_MGC\_21"  
 /tissue\_type="choriocarcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: placenta; Vector: pOTB7; Site\_1: XhoI;

Site\_2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAGGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 272 a 282 c 344 g 203 t  
 ORIGIN

Query Match 43.6%; Score 98; DB 10; Length 1101;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-39;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCTGTGATCTTCAGCAAGCTTCGGATTCCTTTGGCATCGAGCTGATG 69  
 Db 603 CCTGTGATCTTCAGCAAGCTTCGGATTCCTTTGGCATCGAGCTGATG 662

QY 70 GAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCAC 107  
 Db 663 GAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCAC 700

RESULT 15  
 BG718421  
 LOCUS BG718421 768 bp mRNA linear EST 08-MAY-2001  
 DEFINITION 602696451F1 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:4828429 5',  
 mRNA sequence.  
 ACCESSION BG718421  
 VERSION BG718421.1 GI:13997608  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 768)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM10746 row: f column: 14  
 High quality sequence stop: 759.

## FEATURES

Location/Qualifiers  
 1..768  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4828429"  
 /clone\_lib="NIH\_MGC\_97"  
 /lab\_host="DH10B"  
 /note="Organ: testis; Vector: pBluescriptR (modified  
 pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcga  
 ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',  
 size-selected for average insert size 2.2 kb and  
 normalized to 50 ng. This is a primary library enriched  
 for full-length clones and constructed using the  
 Cap-trapper method (Carninci, in preparation). Library  
 constructed by M. Brownstein (NHGRI/NIH), National  
 Institutes of Health). Note: this is a NIH\_MGC Library."

BASE COUNT 154 a 225 c 236 g 152 t  
 ORIGIN

Query Match

41.3%; Score 93; DB 10; Length 768;

Best Local Similarity 100.0%; Pred. No. 4.3e-37;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CAAAGCTTCCGATTCCTTGGCAGCTGCTTTGGCATCGAGCTGATGGAAGTGGACCCCAT 83  
 Db 649 CAAAGCTTCCGATTCCTTGGCAGCTGCTTTGGCATCGAGCTGATGGAAGTGGACCCCAT 708

QY 84 CGGCCACGCTGTACATCTTTGGCACCTGCTGGG 116  
 Db 709 CGGCCACGCTGTACATCTTTGGCACCTGCTGGG 741

Search completed: May 24, 2002, 03:14:10  
 Job time: 5979 sec





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